

=> d que

L4 72 SEA FILE=HCAPLUS ABB=ON PLU=ON ("BARRY C"/AU OR "BARRY C C"/AU OR "BARRY C D"/AU OR "BARRY C DAVID"/AU OR "BARRY C E"/AU OR "BARRY C E III"/AU OR "BARRY C J"/AU OR "BARRY C L"/AU OR "BARRY C M"/AU OR "BARRY C M F"/AU OR "BARRY C MARVIN"/AU OR "BARRY C N"/AU OR "BARRY C P"/AU OR "BARRY C S"/AU OR "BARRY CAROLINE"/AU OR "BARRY CAROLYN B"/AU)

L5 126 SEA FILE=HCAPLUS ABB=ON PLU=ON ("BOUGUELERET L"/AU OR "BOUGUELERET LYDIE"/AU)

L6 130 SEA FILE=HCAPLUS ABB=ON PLU=ON ("CHUMAKOV I"/AU OR "CHUMAKOV I F"/AU OR "CHUMAKOV I M"/AU OR "CHUMAKOV I R"/AU OR "CHUMAKOV I S"/AU OR "CHUMAKOV I V"/AU OR "CHUMAKOV ILYA"/AU OR "CHUMAKOV ILYA M"/AU)

L7 12 SEA FILE=HCAPLUS ABB=ON PLU=ON (L*** OR L*** OR L***)

L8 27 SEA FILE=HCAPLUS ABB=ON PLU=ON (L4 AND (L5 OR L6 OR L7)) OR (L5 AND (L6 OR L7)) OR (L6 AND L7)

L9 302 SEA FILE=HCAPLUS ABB=ON PLU=ON (L4 OR L5 OR L6 OR L7)

L10 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L9 AND BAP?

L11 23 SEA FILE=HCAPLUS ABB=ON PLU=ON L9 AND PROSTAT?

L12 37 SEA FILE=HCAPLUS ABB=ON PLU=ON L8 OR (L10 OR L11)

=> d ibib abs 1-37

L12 ANSWER 1 OF 37 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2006:367166 HCAPLUS
 DOCUMENT NUMBER: 144:405904
 TITLE: Polynucleotides encoding human TBC-1 protein,
 polymorphic markers therein, and uses thereof
 INVENTOR(S): Blumenfeld, Marta; Bougueleret, Lydie;
 Chumakov, Ilya
 PATENT ASSIGNEE(S): Genset S.A., Fr.
 SOURCE: U.S. Pat. Appl. Publ., 114 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2006084073	A1	20060420	US 2004-970750	20041020
PRIORITY APPLN. INFO.:			US 2004-970750	20041020

AB The invention concerns genomic and cDNA sequences of the human TBC-1 gene. The invention also concerns polypeptides encoded by the TBC-1 gene. The invention also deals with antibodies directed specifically against such polypeptides that are useful as diagnostic reagents. The invention further encompasses biallelic markers of the TBC-1 gene useful in genetic anal. The TBC-1 gene is located in a candidate region for prostate cancer on chromosome 4. Expression of TBC-1 gene leads to production of at least two mRNA mols. which have different first exons, exon 1 and 1bis, due to alternative splicing.

L12 ANSWER 2 OF 37 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:182920 HCAPLUS
 DOCUMENT NUMBER: 142:258503
 TITLE: Secreted polypeptide species in human plasma,
 detection assays for smaller proteins and tryptic
 peptides, and expression profiles useful for disease

OM protein - protein search, using sw model	GenCore version 5.1.9			
Run on:	Copyright (c) 1993 - 2006 Bioceleration Ltd.			
	June 29, 2006, 00:41:09 ; search time 110.097 Seconds			
Sequence:	(without alignments) 6765.010 Million cell updates/sec			
Scoring table:	BLOSUM62			
Searched:	Gapop 10.0 , Gapext 0.5			
Total number of hits satisfying chosen parameters:	2599679			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Maximum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	A_GeneSeq_8;*			
	1: geneseqp1980s;*			
	2: geneseqp1990s;*			
	3: geneseqp2000s;*			
	4: geneseqp2001s;*			
	5: geneseqp2002s;*			
	6: geneseqp2003abs;*			
	7: geneseqp2003bs;*			
	8: geneseqp2004s;*			
	9: geneseqp2005s;*			
	10: geneseqp2006s;*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
	SUMMARIES			
Result No.	Score	Query Match Length	DB ID	Description
1	8212	100.0	2144	AAB85029
2	8212	100.0	2144	ADQ89800
3	8204	99.9	2144	AEE02529
4	8195	99.8	2144	ADS34902
5	7635	93.0	2044	ADS34907
6	7627.5	92.9	1569	ABG1232
7	7266	88.5	2036	ADS34903
8	7266	88.5	2036	ADS34904
9	7266	88.5	2036	ADS34904
10	3694	45.0	734	AEC87545
11	3546.5	43.2	1229	ADQ6400
12	3546.5	43.2	1229	AEE02884
13	3102	37.8	9	ADE08012
14	2824.5	34.4	1149	ADU0573
15	2824.5	34.4	1149	ADU40582
16	1918	23.4	897	ADQ96220
17	1916	23.3	897	ADQ96152
18	1914	23.3	897	ADQ96218
19	1603	23.5	8	ADQ66400
20	1603	19.5	325	9
21	1396.5	17.0	4	ABD65342
22	1396.5	17.0	8	ADQ89006
23	705.5	8.6	1798	ABJ26330

				RESULT 1
				AAB85029
			ID	AAB85029 standard; protein; 2144 AA.
			XX	
			AC	AAB85029;
			XX	
			DT	06-AUG-2001 (first entry)
			XX	
			DE	Protein encoded by BAP28 cDNA consisting of exons 1 to 45.
			XX	
			KW	BAP28; prostate; tumour; cancer; diagnostic; genetic analysis.
			XX	
			OS	Homo sapiens.
			XX	
			PH	Key location/Qualifiers
			PT	Misc-difference 1694 /label= Ser or Asn
			PT	Misc-difference 1854 /label= Ala or Val
			PT	Misc-difference 1967
			PT	Misc-difference /label= Asp or Asn
			PT	Misc-difference 2017 /label= Gly or Glu
			PT	
			PN	WO2010066642.
			XX	
			PD	04-JAN-2001.
			XX	
			PF	23-JUN-2000; 2000W0-IB00183.
			XX	
			PR	25-JUN-1999; 90US-014132P.
			PR	18-JAN-2000; 2000US-0176880P.
			XX	
			PA	WPI; 2004-367032/38.
			XX	
			PA	(GST) GENSSET
			XX	
			PT	Barry C Bouquerel et L, Chumakov I, Cohen-Akenine A;
			XX	
			DR	WPI; 2004-367032/38.
			XX	
			PT	New BAP28 poly nucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
			XX	
			PS	Claim 14; Page 297-304; 349pp; English.
			XX	

The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3', and 5', ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polynucleotides and polypeptides have been found to be over expressed in prostate tumor cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are encoded by a first cDNA sequence of the BAP28 gene consisting of the exons 1 to 45

CC CC CC CC

GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 00:42:00 ; Search time 39.2894 Seconds
(without alignments)

Title: US-09-603-665-5_COPY_1_1629
Perfect score: 8212

Sequence: 1 MTSLAQQLQRLLALPQSDASL.....NPPLPSVRRKALDLANKLQQ 1629

Scoring table: BiOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB ID	Description
1	673.5	8.2	1649	2 T39938	hypothetical protein SPBC23E6_04C - fission yeast (Schizosaccharomyces pombe)
2	654	8.0	1769	2 S53378	C;Species: Schizosaccharomyces pombe
3	536	6.5	1650	2 T37864	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
4	248	3.0	2570	2 T37919	C;Accession: T39938 R;Wood, V.; Ralandream, M.A.; Barrel, B.G.; Pohl, T. submitted to the EMBL Data Library, May 1998
5	241	2.9	2895	2 H83362	A;Reference number: Z21892
6	229	2.8	2059	2 T31933	A;Accession: T39938
7	228	2.8	3433	1 S28381	A;Status: Preliminary; translated from GB/EMBL/DBJ
8	228	2.8	4131	2 T21088	A;Molecule type: DNA
9	227.5	2.8	2954	2 T34156	A;Residues: 1-649 <HOO>
10	226	2.8	1447	2 R32150	A;Cross-references: UNIPROT:050179; UNIPARC:UPI000013AF93; EMBL:AL023287; PIDN:CA18872.1
11	226	2.8	1830	2 E83909	A;Experimental source: strain 972b; cosmid c23E6
12	224	2.7	2297	2 A32494	A;Genetics:
13	219.5	2.7	2819	2 A90551	A;Gene: SPBC23E6_04C
14	215	2.6	2663	1 S28261	A;Map position: 2
15	212.5	2.6	4385	2 T39042	Query Match 8.2%; Score 673.5; DB 2; Length 1649;
16	212	2.6	2108	2 S74173	Best Local Similarity 20.5%; Pred. No. 1.7e-25; Matches 348; Conservative 263; Mismatches 490; Indels 53; Gaps 61;
17	210.5	2.6	2269	2 T38677	Description
18	209	2.5	2401	2 T38676	Qy 2 TSLAQLQRLALPQSDASLRLRDEV---ASLIFDRKEAATIDRDTAFAIGCTGLEELIGI 58
19	208	2.5	4717	2 T15181	Db 3 SSIQOKQKNI---QSN-NVULKINKIRKAPSLYDPKVAADMDEEYVTAVSGFHFELAVH 58
20	207.5	2.5	1655	2 S47446	Qy 59 DPSPEQFAPPLFSQALKTLRSVQTKAVNKQDNLNSFLIHLSPYFLLKPAQCKLWLI 118
21	207.5	2.5	4859	2 S74173	Db 59 ERLLYFETKTLQEYQSVQYDVLINRNEKIDLCVQILAPFTETKNAKVLWLI 118
22	207	2.5	3744	2 S46715	Qy 119 HAPHTHYNQOSLIAQCLVPLVYTRIFVRLVQIYKINNSKHRMFWLILPVVKOSCPVAKGLI 178
23	206	2.5	1919	2 T40032	Db 119 RRSIHEVYSDIFSLKIPFDHPFARILGSK-PKSRPFLLENIAKMP-VTISRADI 176
24	204	2.5	3187	2 JC83377	Qy 179 ITCYKOLGFMDFICSLVTKSYKVEAYPGSSAQLRVILAYASTIVSALVAEDVSDN- 237
25	202.5	2.5	4734	2 S47334	Db 230 NYLIDREFLRLYSVAVSVYSSI-DPQIAGMFLSIAASLPLSPSIIPPLVSAITDRLSP- 287
26	202	2.5	3079	1 RGSY12	Qy 294 PSLIKDGSLCILVLU-----ORQKPSLGL 317
27	201.5	2.5	2672	2 A48216	Db 288 -DNIKPALICVHQLQPCSSSEFDHOLEKRSFGASSLILBSQEBRHLDRFVSYWSL 346
28	2.4	2.4	1957	2 T39077	Qy 318 -----KCPFPHICNVNPDLITIHLGISBTYDPLRMLPLVLSIITHVGETEGMD 372
29	199.5	2	1964	2 A59282	Db 347 IKSRKQDKKRLISLD-TSISQIRVTHEQAKFPLSVIP-----VNQDPKAL- 392
					Qy 373 QTVKRHLBAILTKISLKNNDLILLASLIFEEVITYSSQOBEDSNKVSLNNEQFLPLIRL 432

ALIGNMENTS

RESULT 1

T39938
hypothetical protein SPBC23E6_04C - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39938
R;Wood, V.; Ralandream, M.A.; Barrel, B.G.; Pohl, T.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21892
A;Accession: T39938
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-649 <HOO>
A;Cross-references: UNIPROT:050179; UNIPARC:UPI000013AF93; EMBL:AL023287; PIDN:CA18872.1
A;Experimental source: strain 972b; cosmid c23E6
C;Genetics:
A;Gene: SPBC23E6_04C
A;Map position: 2

Query Match 8.2%; Score 673.5; DB 2; Length 1649;

Best Local Similarity 20.5%; Pred. No. 1.7e-25; Matches 348; Conservative 263; Mismatches 490; Indels 53; Gaps 61;

Qy 2 TSLAQLQRLALPQSDASLRLRDEV---ASLIFDRKEAATIDRDTAFAIGCTGLEELIGI 58

Db 3 SSIQOKQKNI---QSN-NVULKINKIRKAPSLYDPKVAADMDEEYVTAVSGFHFELAVH 58

Qy 59 DPSPEQFAPPLFSQALKTLRSVQTKAVNKQDNLNSFLIHLSPYFLLKPAQCKLWLI 118

Db 59 ERLLYFETKTLQEYQSVQYDVLINRNEKIDLCVQILAPFTETKNAKVLWLI 118

Qy 119 HAPHTHYNQOSLIAQCLVPLVYTRIFVRLVQIYKINNSKHRMFWLILPVVKOSCPVAKGLI 178

Db 119 RRSIHEVYSDIFSLKIPFDHPFARILGSK-PKSRPFLLENIAKMP-VTISRADI 176

Qy 179 ITCYKOLGFMDFICSLVTKSYKVEAYPGSSAQLRVILAYASTIVSALVAEDVSDN- 237

Db 230 NYLIDREFLRLYSVAVSVYSSI-DPQIAGMFLSIAASLPLSPSIIPPLVSAITDRLSP- 287

Qy 294 PSLIKDGSLCILVLU-----ORQKPSLGL 317

Db 288 -DNIKPALICVHQLQPCSSSEFDHOLEKRSFGASSLILBSQEBRHLDRFVSYWSL 346

Qy 318 -----KCPFPHICNVNPDLITIHLGISBTYDPLRMLPLVLSIITHVGETEGMD 372

Db 347 IKSRKQDKKRLISLD-TSISQIRVTHEQAKFPLSVIP-----VNQDPKAL- 392

Qy 373 QTVKRHLBAILTKISLKNNDLILLASLIFEEVITYSSQOBEDSNKVSLNNEQFLPLIRL 432

Db 393 QSYRFLDLSVIOPPERKEKGKDNLNITL-----ODKKKSTTSKKDREVL----- 436
 QY ESKYPRTLDVVLVEHHLKETADLKKQELPHQFVSLSTSGKYQFLADSSTSLMSLNPLA 492.
 Db 437 -----LKKSEIDTSQTSFQCLAYADSA-----ADLSSVFSL----- 470
 QY 493 PVRILLAMHHLKKIMKTSKEGVDBSFKEAVLARGDDNIDVLSAISAFEFKEHFSSEV 552
 Db 471 -----LSRKG-DKPELFFCA-----NGSERI 492
 QY 553 TISNLNLNIFORAEISKNGEWEVVIKAADILIKEELISBNDQNSQVVCLOPFFV--IN 610
 Db 493 IILSIEL-----RKTIEENKDWDYQII--LPVNLVLSQ 524
 QY 611 NDDPTEAEMKIAIYLSKSGICSLHPLLRGWEALENVIKSTKBGKLIGVANGKMEIELAD 670
 Db 525 SKDTEVRSRALNLT-----PFLERNE 547
 QY 671 NINLGDPFSSMLKNGEDLISVGEEBESPNLKQKQVTPHVLISVLVSCSSLKETHFPFAIRVF 730
 Db 548 NL-----EFSIYGMDDND-----DGTYLF 596
 QY 731 SLLQKKKKLSEITAVIPSEHMLDRGIVPELNAHYVEELNSTORVAVEDSVFLV 790
 Db 563 ---KOLRWLSPET-----KYYCSDDLJLDRSSEIGL----- 562
 QY 791 FSLKKFTIYALKAPSKFKGDIWNPQLKEDSRDYLHLLIGLFEMMLNGADAVHFRVLMK 850
 QY 597 SIFERLFTTEKKFNAK-----EIAVT 619
 Db 851 LFKVHHLDFVQFLFKFCSVLWTVGSSLISNPLNCVSKVTLQTOALYVFCAMLSQKQCKH 910
 QY 620 SFLSH-----AACSKLN----- 633
 Db 911 QLASSISSPVVTSLLNLNGSPVKEVRRAIQCLOLSCVASPFVLLHHLISREITSDA 970
 QY 634 -----VTRVLLIEILTRVHG-----KVED----- 651
 Db 971 AYVITQDLATLFEELQREKKLKHQKLSERTLKLNLSCVSCPSVIAKOLMKVITQGVNGEMV 1030
 QY 652 ---AKQKILLPPLQSEFNS-EKEKVKSCREVAEVLNGCFNHTS--FTSISLSESSNIV 704
 Db 1031 LSQOLPMAEQLKKIQCQETAVLKDTEAMVHLHTLGKYNFESVSLNEDPKSLDIFIKRH 1090
 QY 705 LSCAR--CRRIVE--IOS-----HL-----KDPORL-FVKAVI 733
 QY 1091 TTKELYAGMPTIQTAKEKTFPEFAISDEKQVQKULMLDLYVCKNSICAQTVSS 1150
 Db 734 SODE---OPHYTVVDLSDKIP-----DTV 755
 Db 1151 FKGISVNAEQRVTELEPPDKAKLGLTVOOKRQKMQKKSQDLSVQEVGGSYWQRTL 1210
 QY 756 PK-----KLGSVVLUKEKPNPATAKRKIDS-HIFDSDYRTRI 794
 Db 1211 LEIJOHKKKLRSPOQILVPTLNLSRCLEPLPQEOGNNYTKQKLLSCLLN----CQK 1265
 QY 795 UEBETKQAAASYPKLASF-LFEVILNSVI-ALKEDIVSSNLYQOLLGIVENIGASRTE 852
 QY 1266 LSFDGGKLPKDIIDEEKENVELLVQCTRLSEMOPTHHLALLGTVAGIFPDVKLHIMS 1325
 Db 853 LSP-----SIRDTLWGCIRSTNNPQIQNQKALLYVSLANAAPEAVLHGSMP 899
 Db 1326 ITPFMGAMVNRDQDTSQVINKTQVTPMIALQ--SPSGDSTEVSRVNEETVVKITSVF 1383
 QY 900 ITPFMGSTVLSRDRDASFHVQVKWISALLRKGFDSS-----LVSFC 947
 QY 1384 VDALPHVPHERRFLPILVOLVDTGAEKELWILLLFFQVTKVLAAYGKDALLEAD 1443
 QY 948 VNAFPHTPQHRRRLYRVLQIGNSRLSVLVI---QFAEMLLA----KSTNTVVAI 998
 QY 1444 TEFWSVSCFVQHQLOQISMLNTIQLYLKPEK--BETIPKAWFSNKESEOBMLQVN 1501

Db 999 HDPCFLTVQFSVADRGISINQCSRFCLKSLSBEOQSNSDNCNSKAVSLIKLDELP----MD 1053
 QY 1502 VETHTSKOLRHPKFPLSVFMMQOLLSSNNF--LKKVVEGCPPEIKGLEERULETWTGTY 1558
 Db 1054 VOLATLGLSR-VKVLRL--ISLVSKAKNPFDLAKIMENSDSFVR-IQAGLFESKLII 1109
 QY 1559 SAVAQS--MERNADKLTVKFWRALLSKAVDLDKUNALPPTETFIPVIRGLVGNPLPSV 1615
 Db 1110 TLUQOSSNEME-----LGHVVYALRSVTHLPLNLFCTVLGULHDERALL 1155
 QY 1616 RKKALDLANKLQQ 1629
 Db 1156 REKALSTVQQRVQ 1169

RESULT 2

S53378 probable membrane protein YJL109c - Yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein J0808

C;Species: *Saccharomyces cerevisiae*

C;Date: 05-May-1995 #Sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S53378; S53379

R;Rasmussen, S.W.

Submitted to the EMBL Data Library, February 1995

A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and C

A;Reference number: S53376

A;Accession: S53378

A;Molecule type: DNA

A;Residues: 1-769 <RAS>

A;Cross-references: UNIPROT:P42945; UNIPARC:UPI0000052F40; EMBL:X85021; NID:9728698; PID:

A;Reference number: S56876

A;Accession: S56887

A;Molecule type: DNA

A;Residues: 1-769 <RAW>

A;Cross-references: UNIPARC:UPI0000052F40; EMBL:Z49384; NID:91008292; PID:G1008293; MIPS:

R;Rasmussen, S.W.

Year: 11, 873-893, 1995

A;Title: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3

A;Reference number: S57357; MNUID:96090136; PMID:4783851

A;Status: nucleic acid sequence not shown; translation not shown

A;Accession: S57359

A;Molecule type: DNA

A;Residues: 1-1769 <RAF>

A;Cross-references: UNIPARC:UPI0000052F40; EMBL:X85021; NID:9728698; PID:CAA59385.1; PII

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

C;Generics:

A;Cross-references: SGD:S0003645

A;Map position: 10L

C;Keywords: transmembrane protein

Query Match 8.0%; Score 654; DB 2; Length 1769;
 Best Local Similarity 20.8%; Pred. No. 1.7e-24; Gaps 65;
 Matches 366; Conservative 252; Mismatches 542; Indels 598; Gaps 65;
 QY 1 1 MTSIADQOLRILALPQDASL---ISRDEVAISLFLDPKEAATIDRTAFAIGCTGIEELL 56
 Db 1 MSSLSDQLAQKASNNATVALDKRKKLHSASLINSKTAQDQDFIFENASKALEELS 60
 QY 57 GIDPSDEQFAPLPSLAQKTERSTVKVAKNQDLSLTHLSPYFLPKPAQKCLEW 116
 Db 61 QIEPKFAIFSRFLFSESSISLDRNVQKEETKDLKNAIVAYLASSKWWIAPTHAEW 120
 QY 117 LIHRFHILHYQDLSIACVLPYHEMIFVRYIQKINNSHRFWLPL-----VK 167
 Db 121 LYTRFHVHQVTEMLLSTUNYQTYEVKRIISIK-----LPPFLNCISNFVR 169
 QY 168 QGVPLAKGTLITHCYKDLGMDIFCSLNLVTSVVKFAEYPSQAQRLVLAAYFASIVS 227
 Db 170 SKPPTAL-TM-KLNDMPLKLYTSDQCIKATYHQ-----LIFTCCFIN- 219
 QY 228 LVAABDVSDNITAKLFPYI---QKGKSSIPDYRATYMIQCOISVKTMENTVNSLA 283

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model
Run on: June 29, 2006, 00:41:34 ; Search time 166.656 Seconds
(without alignments)

941.668 Million cell updates/sec

Title: US-09-603-665-5_COPY_1_1629
Perfect score: 8212

Sequence: 1 MTSLAQDILQLALPQSDASL.....NPPLPSVRKALDILNNKLQQ 1629

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing First 45 summaries

Database: UniProt 7.2;*
1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Query % Match length DB ID Description

Result No.	Score	Query	Match length	DB	ID	Description
1	8204	99.9	2144	1	HEATR_HUMAN	09h583 homo sapien
2	7755.5	94.4	2063	2	05T3Q7_HUMAN	05t3q7 homo sapien
3	4891	94.4	1180	2	03UNW7_MOUSE	03unw7 mus musculus
4	4516	55.0	1090	2	03TNB6_MOUSE	03tnb6 mus musculus
5	4118	50.1	2159	2	07SY48_BRARE	07sy48 brachychaenio
6	4072	49.6	984	2	03TMK0_MOUSE	03tmk0 mus musculus
7	3589	43.7	2288	2	04T7Z3_TETNG	04t7z3 tetraodon n
8	3099	37.7	733	2	08BLJ4_MOUSE	08bj4 mus musculus
9	3095	37.7	733	2	03T910_MOUSE	03t910 mus musculus
10	2973	36.2	1106	2	06P197_HUMAN	06p197 homo sapien
11	2298	1278	2	07T152_BRARE	07t152 brachychaenio	
12	2298	28.0	1336	2	07T152_BRARE	07t152 brachychaenio
13	2181.5	26.6	958	1	HEATR_MACFA	09gm44 macaca fasciata
14	1916	23.3	897	2	Q8N7L7_HUMAN	08n7l7 homo sapien
15	1444	17.6	2104	2	07PWDS_ANOGA	07pwds amphotepes g
16	1398.5	17.0	2096	2	06AWS5_DROME	06aws5 drosophila
17	1396.5	17.0	2096	1	HEATR_DROME	09m15 drosophila
18	948.6	11.6	743	2	03V1X6_MOUSE	03v1x6 mus musculus
19	852	10.4	168	2	02K1F5_BOVIN	02k1f5 bos taurus
20	832	10.1	2251	2	Q4P937_USTMA	Q4p937 ustulago ma
21	809.5	9.9	2087	2	Q8T9E7_DROME	08t9e7 drosophila
22	799.5	9.7	2237	2	054M1L_DICDI	054ml4 drosophila
23	786.5	9.6	1830	1	HEATR_ARATH	09c834 arabidopsis
24	774	9.4	2021	2	05KBQ2_CRYNE	05kbq2 cryptococci
25	767	9.3	2021	2	Q55NB7_CRYNE	055nb7 cryptococcus
26	763.5	9.3	1857	2	Q6BXQ5_DEBHA	06bxq5 debaryomyces
27	1801	9.2	1801	2	Q5B1X5_EMENT	05b1x5 aspergillus
28	757.5	9.2	2122	2	Q5CAF8_ORYSA	05caf8 oryza sativa
29	715.5	8.7	1802	2	Q2ULC5_ASPRO	02ulc5 aspergillus
30	707.5	8.6	1770	2	Q6FT93_CANGA	06ft93 candida glauca
31	707.5	8.6	1798	2	Q4WL19_ASPPU	04wl19 aspergillus

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OC: Homo
RN: NCBI_TaxID=9606;
RP: GLY-2017.
RA: Bougueleret L, Chumakov S, Barry J, Cohen-Akenine A.;
RT: "A novel BAP28 gene and protein."
RL: Patent number WO200706659, 04-JAN-2001.
RN: [1]
RP: NUCLEOTIDE SEQUENCE AND VARIANTs-SER-1694; ALA-1854; ASP-1967 AND
Human chromosome 1 international sequencing consortium;
RL: Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN: [3]
RP: NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1771-2144.
Pubmed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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OM protein - protein search, using sw model

Run on: June 29, 2006, 00:46:09 ; Search time 28.4956 Seconds
 (without alignments)
 5003.834 Million cell updates/sec

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Scoring table: BL05IM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RR_COMBO_pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfiles1.pep:
 *

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	310	3.8	200	2 US-09-248-796A-15108 Sequence 15108, A Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
2	228	2.9	3433	2 US-09-091-501B-10 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
3	228	2.8	3433	2 US-09-1538-092-1136 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
4	227.5	2.8	2954	3 US-09-724-584-1 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
5	227.5	2.8	3830	2 US-09-693-205A-4 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
6	222.5	2.7	3829	2 US-09-693-205A-16 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
7	216.5	2.6	2663	2 US-09-538-092-1352 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
8	215	2.6	3829	2 US-09-693-205A-2 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
9	214.5	2.6	2662	2 US-09-595-684B-31 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
10	212	2.6	2108	2 US-09-538-092-87 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
11	206.5	2.5	1786	2 US-08-973-462-8 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
12	206.5	2.5	2482	1 US-08-328-254-6 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
13	206.5	2.5	3248	1 US-08-353-700-1 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
14	206.5	2.5	3249	1 PCT-US95-16216-1 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
15	206.5	2.5	3210	2 US-09-538-092-154 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
16	203.5	2.5	3066	2 US-08-952-127-12 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
17	202	2.5	3066	2 US-08-949-016-6368 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
18	201.5	2.5	1979	2 US-09-949-016-7404 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
19	201.5	2.5	2047	2 US-09-949-016-7404 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
20	201.5	2.5	10182	2 US-09-134-001C-3159 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
21	198	2.4	3079	5 PCT-US94-00198-4 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
22	197.5	2.4	2186	5 PCT-US94-00198-4 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
23	197.5	2.4	2349	2 US-09-538-092-914 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
24	194	2.4	4872	2 US-09-942-783-3 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
25	194	2.4	2516	2 US-09-949-016-0280 Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans
26	2.4	3056	1 US-08-508-836A-8	Sequence 38, B Sequence 10, Appli Sequence 1136, Ap Sequence 1, Appli Sequence 4, Appli Sequence 16, Appli Sequence 200, Appli Organism: Candida albicans

RESULT 1

US-09-248-796A-15108

; Sequence 15108, Application US/09248796A
 ; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248, 796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIORITY APPLICATION NUMBER: US 60/074, 725
 ; PRIORITY FILING DATE: 1998-02-13
 ; PRIORITY FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO: 15108
 ; LENGTH: 200
 ; TYPE: PRT
 ; ORGANISM: Candida albicans

ALIGNMENTS

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US-09-248-796A-15108

; Sequence 15108, Application US/09

APPLICANT: Davies, Kay E
 TITLE OF INVENTION: Utrophin gene expression
 FILE REFERENCE: 620-42
 CURRENT APPLICATION NUMBER: US/09/091,501B
 CURRENT FILING DATE: 1998-06-18
 PRIORITY APPLICATION NUMBER: PCT/GB96/03156
 PRIORITY FILING DATE: 1996-12-19
 PRIORITY APPLICATION NUMBER: GB 9525962.8
 PRIORITY FILING DATE: 1995-12-19
 PRIORITY APPLICATION NUMBER: GB 9615197.9
 PRIORITY FILING DATE: 1996-07-26
 PRIORITY APPLICATION NUMBER: GB 9622174.2
 PRIORITY FILING DATE: 1996-10-24
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 10
 LENGTH: 3433
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 LOCATION: misc feature
 NAME/KEY: misc feature
 OTHER INFORMATION: Description of Artificial Sequence: Full length
 OTHER INFORMATION: utrophin construct; Xaa = unknown
 US-09-091-501B-10

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 Best Local Similarity 18.7%; Pred. No. 8-3e-09;
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 Sequence 1136, Application US/09538092

OM protein - protein search, using sw model
Run on: June 29, 2006, 00:52:34 ; Search time 101.893 Seconds
Copyright: (c) 1993 - 2006 Biocceleration Ltd.
GenCore version 5.1.9

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Gapp 10.0 , Gapext 0.5

Scored: 2097797 seqs, 46314858 residues
Total number of hits satisfying chosen parameters: 2097797
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

Result No.	Score	Query Length	DB ID	Description
1	8212	100.0	2144	5 US-10-745-237-230 Sequence 23.0, APP
2	8195	99.8	2144	6 US-11-124-368A-277 Sequence 27.7, APP
3	87635	93.0	2044	6 US-11-124-368A-278 Sequence 27.8, APP
4	7627.5	92.9	1569	5 US-10-450-763-45591 Sequence 45.591, APP
5	7256	88.5	2036	6 US-11-14-368A-276 Sequence 27.6, APP
6	7266	88.5	2036	6 US-11-124-368A-280 Sequence 28.0, APP
7	8826	88.5	2036	6 US-11-124-368A-281 Sequence 28.1, APP
8	3694	45.0	734	4 US-10-128-260A-3300 Sequence 33.0, APP
9	2824.5	34.4	1149	5 US-10-128-558-567 Sequence 16.7, APP
10	1916	23.3	897	4 US-10-764-425-177 Sequence 17.7, APP
11	1503	19.5	325	5 US-10-764-558-358 Sequence 35.8, APP
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20	379	9.5	92	4 US-10-424-599-248111 Sequence 248111, APP
21	228	2.8	3433	4 US-10-408-765A-731 Sequence 731, APP
22	228	2.8	3433	4 US-10-408-765A-732 Sequence 732, APP
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24	228	2.8	4131	4 US-10-369-493-5316 Sequence 5136, APP
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27	2.7	2543	5 US-10-828-985A-9 Sequence 9, APP	

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cell updates/sec

DLIANKLUQQ 1629

7797

RESULT 1
US-10-745-237-230
Sequence 230 Application US/10745-237
Publication No. US200505227301A1
GENERAL INFORMATION:
APPLICANT: ~~Excalibur Limited~~
APPLICANT: Bell, Graham
APPLICANT: Frenz, Lisa
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: P015819N0 CYK
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US 60/468,402
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: PatentIn version 3.1
SEQ ID NO 230
SEQUENCE: Sequence 230, APP
SEQUENCE: Sequence 277, APP
SEQUENCE: Sequence 278, APP
SEQUENCE: Sequence 45591, A
SEQUENCE: Sequence 276, APP
SEQUENCE: Sequence 280, APP
SEQUENCE: Sequence 281, APP
SEQUENCE: Sequence 3300, APP
SEQUENCE: Sequence 167, APP
SEQUENCE: Sequence 177, APP
SEQUENCE: Sequence 358, APP
SEQUENCE: Sequence 36, APP
SEQUENCE: Sequence 22518, A
SEQUENCE: Sequence 3388, APP
SEQUENCE: Sequence 3388, APP
SEQUENCE: Sequence 1616, APP
SEQUENCE: Sequence 189782, APP
SEQUENCE: Sequence 2412, APP
SEQUENCE: Sequence 37036, A
SEQUENCE: Sequence 248111, APP
SEQUENCE: Sequence 731, APP
SEQUENCE: Sequence 732, APP
SEQUENCE: Sequence 5681, APP
SEQUENCE: Sequence 5136, APP
SEQUENCE: Sequence 1, APP
SEQUENCE: Sequence 1335, APP
SEQUENCE: Sequence 9, APP

Description

ALIGNMENTS

218 2.7 2665 6 US-11-124-368A-214 Sequence 214, APP
218 2.7 2668 6 US-11-124-368A-215 Sequence 215, APP
217.5 2.6 2228 5 US-10-511-096-2 Sequence 2, Appli
217.5 2.6 2230 5 US-10-511-096-4 Sequence 4, Appli
216 2.6 2250 5 US-10-511-096-6 Sequence 6, Appli
216 2.6 2252 5 US-10-511-096-8 Sequence 8, Appli
215.5 2.6 2503 5 US-10-828-985A-11 Sequence 11, Appli
215 2.6 2568 5 US-10-828-985A-7 Sequence 7, Appli
215 2.6 2633 5 US-10-450-763-36864 Sequence 3684, A
215 2.6 2663 5 US-10-723-850-749 Sequence 749, APP
214.5 2.6 3829 4 US-10-408-765A-849 Sequence 849, APP
214.5 2.6 5 US-10-723-860-2137 Sequence 2137, APP
213 2.6 1581 4 US-10-437-963-196981 Sequence 196981, APP
212 2.6 2108 4 US-10-369-493-1537 Sequence 1537, APP
210.5 2.6 2153 6 US-11-097-141-9003 Sequence 9003, APP
205.5 2.5 1786 3 US-09-742-096-3 Sequence 3, Appli
206.5 2.5 1786 6 US-11-198-400-3 Sequence 3, Appli
206.5 2.5 1787 4 US-10-415-253-2 Sequence 2, Appli

Db 241 KLFPIYIQGKLSIIPDRAATMICOISVKVMENTFVNSLASQIQLIKTIPSLIKD 300
 QY 301 LSCIVLQLQROKPPSICKUPPHCNVPDLITHGISETYDPSPLRMLPWHVSIH 360
 Db 301 LSCIVLQLQROKPPSICKUPPHCNVPDLITHGISETYDPSPLRMLPWHVSIH 360
 QY 361 HVTGEGTEGMDGQYKRHLAELTKISLKNLDHLASLFEELYISYSOEEMDSNKYL 420
 Db 361 HVTGEGTEGMDGQYKRHLAELTKISLKNLDHLASLFEELYISYSOEEMDSNKYL 420
 QY 421 LNEFLPLRILLESKIPRILDVWEEHLKEDADJKQELFHQFSLSTSGGKQFLAND 480
 Db 421 LNEFLPLRILLESKIPRILDVWEEHLKEDADJKQELFHQFSLSTSGGKQFLAND 480
 QY 481 TSLMLSLNHLAPYRILAMNHKLKIMTKTSKEGVRSFIKEAVLRLGDDNDVUTSA 540
 Db 481 TSLMLSLNHLAPYRILAMNHKLKIMTKTSKEGVRSFIKEAVLRLGDDNDVUTSA 540
 QY 541 FEIKKEHESSEVT-SNLNLFORABLKSQEWYEVKIAADILKEEILSENDOLSNQV 600
 Db 541 FEIKKEHESSEVT-SNLNLFORABLKSQEWYEVKIAADILKEEILSENDOLSNQV 600
 QY 601 VCLIPFWINDDTBEAEMKIAILSKGICSLHPLRGWEAELENVKSTKPKLIGA 660
 Db 601 VCLIPFWINDDTBEAEMKIAILSKGICSLHPLRGWEAELENVKSTKPKLIGA 660
 QY 661 NQRMIELLADNINGGDPSMILKOMTDELISGEERSFNLKQKVTHVILSVLSCSSIKE 720
 Db 661 NQRMIELLADNINGGDPSMILKOMTDELISGEERSFNLKQKVTHVILSVLSCSSIKE 720
 QY 721 THFPAIRFVSLQKIKKLESVITAVEIPSEWHIELMDRGTEVELWAHYVEELNSTO 780
 Db 721 THFPAIRFVSLQKIKKLESVITAVEIPSEWHIELMDRGTEVELWAHYVEELNSTO 780
 QY 781 VAYEDSVLVEUSLKKFYIYAKAPPSFKPKDIDWNPOLKEDSRSYLHLLGPEMMLGA 840
 Db 781 VAYEDSVLVEUSLKKFYIYAKAPPSFKPKDIDWNPOLKEDSRSYLHLLGPEMMLGA 840
 QY 841 DAVFPRVLMKLFKHLEDYFQKFCFSVILWTCSSLSLPLNCSSVKTQTOALYVGAM 900
 Db 841 DAVFPRVLMKLFKHLEDYFQKFCFSVILWTCSSLSLPLNCSSVKTQTOALYVGAM 900
 QY 901 LSSQTKTOCKHQLASSISSPVTSLINLGSQPKVYERRAOCLOALSGVASPFVILIDH 960
 Db 901 LSSQTKTOCKHQLASSISSPVTSLINLGSQPKVYERRAOCLOALSGVASPFVILIDH 960
 QY 961 SKABEITSRAYVYDQTLFEEOREKLUKSHOKLSETTLKNSCVSCPSYAKDMK 1020
 Db 961 SKABEITSRAYVYDQTLFEEOREKLUKSHOKLSETTLKNSCVSCPSYAKDMK 1020
 QY 1021 VLOCGNGEMLSQLPMAQOLKEIOPAVLQDEAMWHLHTGKMFHVSUINEDPK 1080
 Db 1021 VLOCGNGEMLSQLPMAQOLKEIOPAVLQDEAMWHLHTGKMFHVSUINEDPK 1080
 QY 1081 SLDPIKAVHTKELYAGMPTQITALEKIKTPPAFALSDEKVOQKLLMFDLVLNCN 1140
 Db 1081 SLDPIKAVHTKELYAGMPTQITALEKIKTPPAFALSDEKVOQKLLMFDLVLNCN 1140
 QY 1141 SHCQTVSSVFKGSYNSAQRVILSLEPPDKAKPQGTVQKRRQKQKQSKDLSVQEG 1200
 Db 1141 SHCQTVSSVFKGSYNSAQRVILSLEPPDKAKPQGTVQKRRQKQKQSKDLSVQEG 1200
 QY 1201 GSYWQRTVILELQHKKQLSPQILVPLTFLNLISRCLEPLPQOGNMETQKDLSCU 1260
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 QY 1261 NICOKLSPQGKIKDILBEKFVNLVOCIRSEMPOTHHALLGTVAGFPDKU 1320
 Db 1261 NICOKLSPQGKIKDILBEKFVNLVOCIRSEMPOTHHALLGTVAGFPDKU 1320
 QY 1321 HNINSIFTMGANTMRDDTYSFQVINKTVKMFVPAIQLQSDGSEIEVNRVERIVKII 1380
 Db 1321 HNINSIFTMGANTMRDDTYSFQVINKTVKMFVPAIQLQSDGSEIEVNRVERIVKII 1380

RESULT 2

US-11-124-368A-277

; Sequence 277, Application US/11124368A

; Publication No. US20050287559A1

; GENERAL INFORMATION:

; APPLICANT: Michele Carrill

; APPLICANT: James J Devlin

; APPLICANT: May Luke

; TITLE OF INVENTION: Genetic Polymorphisms Associated with

; Vascular Diseases, Methods of Detection and Uses Thereof

; FILE REFERENCE: CLO1524

; CURRENT APPLICATION NUMBER: US/11/124, 368A

; CURRENT FILING DATE: 2005-05-09

; PRIORITY NUMBER: US 60/58, 845

; PRIORITY FILING DATE: 2004-05-07

; PRIORITY APPLICATION NUMBER: US 60/625, 936

; PRIOR FILING DATE: 2004-11-09

; NUMBER OF SEQ ID NOS: 2112

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 277

; LENGTH: 2144

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-124-368A-277

Query Match 99.8%; Score 8195; DB 6; Length 2144;
 Best Local Similarity 99.8%; P-Pre. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1626; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MTLAQQLQRLAIPQDASLRLSDEVASLFLPDKPEAKTIDRUTAFATCTGQLELIGDP 60
 Db 1 MTLAQQLQRLAIPQDASLRLSDEVASLFLPDKPEAKTIDRUTAFATCTGQLELIGDP 60
 QY 61 SFROPEAPLPSQALKLTERSVOVKANQDENSISLFLHSPYFLIKPAQKCLEWLR 120
 Db 61 SFROPEAPLPSQALKLTERSVOVKANQDENSISLFLHSPYFLIKPAQKCLEWLR 120
 QY 121 FHLHYNQDSLICLVPHTETLFLVYIOLKLNNSKRWRWFLLPVKOSGVPLAKGTLT 180
 Db 121 FHLHYNQDSLICLVPHTETLFLVYIOLKLNNSKRWRWFLLPVKOSGVPLAKGTLT 180
 QY 181 HCYKDGLGMDPCLSLVTKSYKVAEYCGSSAOLRVLAFYASTIVSALVAASVDNIA 240
 Db 181 HCYKDGLGMDPCLSLVTKSYKVAEYCGSSAOLRVLAFYASTIVSALVAASVDNIA 240
 QY 181 HCYKDGLGMDPCLSLVTKSYKVAEYCGSSAOLRVLAFYASTIVSALVAASVDNIA 240
 Db 181 HCYKDGLGMDPCLSLVTKSYKVAEYCGSSAOLRVLAFYASTIVSALVAASVDNIA 240

QY 241 KLFPIYIQGKLSIIPDRAATMICOISVKVMENTFVNSLASQIQLIKTIPSLIKD 300
 Db 1381 SVFDALPHVPEHRLRPLTVQLVDTGAEKFWILLLILFEQVTKTVAAYGEKDIL 1440
 QY 1381 SVFDALPHVPEHRLRPLTVQLVDTGAEKFWILLLILFEQVTKTVAAYGEKDIL 1440
 Db 1441 EATTEFWVCCERSVQHOIQSMLNQIQLKLUPEBKEETIPAVSNKRSSEOBEMQVF 1500
 QY 1441 EATTEFWVCCERSVQHOIQSMLNQIQLKLUPEBKEETIPAVSNKRSSEOBEMQVF 1500
 Db 1501 NVEHTSKOLRHKFLSVMSQDLSUNSPNFKCVCWESGGPELKGLERLETVLGYSA 1560
 QY 1501 NVEHTSKOLRHKFLSVMSQDLSUNSPNFKCVCWESGGPELKGLERLETVLGYSA 1560
 Db 1561 VAOQMERVADKLTVKFWRALLSKAYDLDKVNALLPBTPTPVIRGLVGNPSPVVKAL 1620
 QY 1561 VAOQMERVADKLTVKFWRALLSKAYDLDKVNALLPBTPTPVIRGLVGNPSPVVKAL 1620
 Db 1621 DLANKLQQ 1629
 QY 1621 DLANKLQQ 1629
 Db 1621 DLANKLQQ 1629

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GenCore version 5.1.9

MM protein - protein search, using sw model

run on: June 29, 2006, 00:53:49 ; Search time 9.06679 Seconds

sequence: (without alignments) 4243.670 Million cell updates/sec

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searched: 103426 seqs, 23619683 residues

total number of hits satisfying chosen parameters: 103426

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : Published Applications AA New:*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us06 NEW PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us07 NEW PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us08 NEW PUB.pep:*

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7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us11 NEW PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us60 NEW PUB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

US-11-293-697-3300

; Sequence 3300, Application US/11293697

; Publication No. US20060105376A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/11-293, 697

; CURRENT FILING DATE: 2005-12-05

; PRIOR APPLICATION NUMBER: US/10/108, 260

; PRIOR FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 3300

; TYPE: PRT

; ORGANISM: Homo sapiens

; LENGTH: 734

; US-11-293-697-3300

ALIGNMENTS

Query Match 45.0%; Score 3694; DB 7; Length 734;

Best Local Similarity 100.0%; Pred. No. 1.7e-208; Mismatches 0; Indels 0; Gaps 0

Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Description

Score	Length	DB ID	Sequence
3300	7	US-11-293-697-3300	Sequence 3300, App
325	6	US-10-505-928-335	Sequence 1903, App
3113	6	US-11-301-554-1903	Sequence 51794, App
3125	6	US-10-449-902-51794	Sequence 43305, App
1325	6	US-10-449-902-43305	Sequence 46322, App
1206	6	US-10-449-902-46322	Sequence 784, App
1176	6	US-10-504-973-32	Sequence 47106, App
1171	6	US-10-505-938-784	Sequence 296, App
1170	7	US-11-293-102-956	Sequence 2967, App
1170	7	US-11-293-697-2967	Sequence 45961, App
1170	7	US-10-449-902-45961	Sequence 2929, App
1170	6	US-10-511-937-2929	Sequence 32, App
1170	6	US-10-449-902-47106	Sequence 47146, App
1170	6	US-10-449-902-47146	Sequence 4624, App
1170	6	US-10-471-571A-4624	Sequence 4478, App
1170	6	US-10-486-020-14	Sequence 45516, App
1170	6	US-10-471-571A-4478	Sequence 55021, App
1170	6	US-10-449-902-45516	Sequence 45962, App
1170	6	US-10-449-902-55021	Sequence 227, App
1170	6	US-10-505-928-227	Sequence 4996, App
1170	6	US-10-449-902-4996	Sequence 55428, App
1170	6	US-10-449-902-55428	Sequence 242, App
1170	6	US-10-505-928-257	Sequence 257, App

Sequence 43318, App

Sequence 43257, App

Sequence 34045, App

Sequence 154, App

Sequence 3910, App

Sequence 2968, App

Sequence 2, App

Sequence 155, App

Sequence 7, App

Sequence 102, App

Sequence 140, App

Sequence 142, App

QY 361 HVTGEBTEGMDQIYKRRHAILTISLKNNDLHLLASLAFEEY-SYSSOEMDNKVL 420
 361 HVTGEBTEGMDQIYKRRHAILTISLKNNDLHLLASLAFEEY-SYSSOEMDNKVL 420
 Db 421 LNEQFLPLRILLESKPYRPTDVLVLEBLKETADLKKQELRFQFVALSTSGKYQFLADSD 480
 Qy 421 LNEQFLPLRILLESKPYRPTDVLVLEBLKETADLKKQELRFQFVALSTSGKYQFLADSD 480
 Db 421 LNEQFLPLRILLESKPYRPTDVLVLEBLKETADLKKQELRFQFVALSTSGKYQFLADSD 480
 Qy 481 TSLMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLAVLGGDNDVYLSA 540
 Db 481 TSLMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLAVLGGDNDVYLSA 540
 Db 481 TSLMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLAVLGGDNDVYLSA 540
 Qy 541 FEIPEKHFSSEVTISNLNQFRAEISKNGEWYEVKIADILIKEILSENDQNSQV 600
 Db 541 FEIPEKHFSSEVTISNLNQFRAEISKNGEWYEVKIADILIKEILSENDQNSQV 600
 Db 541 FEIPEKHFSSEVTISNLNQFRAEISKNGEWYEVKIADILIKEILSENDQNSQV 600
 Qy 601 VCLLPFPVVIINDDTSAEMKIAIYISKSGICSLHPLJLPGWEALENVKSTKPGKLIGVA 660
 Db 601 VCLLPFPVVIINDDTSAEMKIAIYISKSGICSLHPLJLPGWEALENVKSTKPGKLIGVA 660
 Db 601 VCLLPFPVVIINDDTSAEMKIAIYISKSGICSLHPLJLPGWEALENVKSTKPGKLIGVA 660
 Qy 661 NORMMELLADNNINGDPPSMKLMKVMDLISYGEEESEPNLKKVYKOTVTEVILSYLVSASSLKE 720
 Db 661 NORMMELLADNNINGDPPSMKLMKVMDLISYGEEESEPNLKKVYKOTVTEVILSYLVSASSLKE 720
 Db 661 NORMMELLADNNINGDPPSMKLMKVMDLISYGEEESEPNLKKVYKOTVTEVILSYLVSASSLKE 720
 Qy 721 THFPAIRVTSLLQ 734
 Db 721 THFPAIRVTSLLQ 734
 Db 721 THFPAIRVTSLLQ 734

RESULT 2

US-10-505-928-325
 ; Sequence 325, Application US/10505928
 ; Publication No. US20060088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505, 928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIORITY APPLICATION NUMBER: US 60/363, 019
 ; PRIORITY FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 325
 ; LENGTH: 3113
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-505-928-325

Query Match 2 5%: Score 206 5; DB 6; Length 3113;
 Best Local Similarity 18 4%; Pred. No. 0.0016; Matches 309; Conservative 294; Mismatches 584; Indels 489; Gaps 75;

Qy 266 CQISKVMTENYVNLASOIIKIKITKIPSLIKDQISCLVLLQKPESLGKPPPHLC 325
 Db 266 CQISKVMTENYVNLASOIIKIKITKIPSLIKDQISCLVLLQKPESLGKPPPHLC 325
 Db 266 CQISKVMTENYVNLASOIIKIKITKIPSLIKDQISCLVLLQKPESLGKPPPHLC 325
 Qy 1425 CQMSKMSLEQTYVSLKAENLVLSTNLNFOGD---LVKEMOGLLEGIL----- 1471
 Db 1425 CQMSKMSLEQTYVSLKAENLVLSTNLNFOGD---LVKEMOGLLEGIL----- 1471
 Db 1425 CQMSKMSLEQTYVSLKAENLVLSTNLNFOGD---LVKEMOGLLEGIL----- 1471
 Qy 326 NVPDLITLHGISETYDVSPLRYMLPHLVSIHVHTGEBTEGMDQIYKRRHAILT 385
 Db 326 NVPDLITLHGISETYDVSPLRYMLPHLVSIHVHTGEBTEGMDQIYKRRHAILT 385
 Db 326 NVPDLITLHGISETYDVSPLRYMLPHLVSIHVHTGEBTEGMDQIYKRRHAILT 385
 Qy 1472 -----VPSLSSCVDSSLSSLG-DSSFRALRQ-TGD 1504
 Db 1472 -----VPSLSSCVDSSLSSLG-DSSFRALRQ-TGD 1504
 Db 1472 -----VPSLSSCVDSSLSSLG-DSSFRALRQ-TGD 1504
 Qy 386 ISLKNNL-----DHLLASLIFEEYISYSS----- 409
 Db 386 ISLKNNL-----DHLLASLIFEEYISYSS----- 409
 Db 386 ISLKNNL-----DHLLASLIFEEYISYSS----- 409
 Qy 1505 MSLUSLNLEGAVSANOCSVDEVFCSSLQEEENLTKTPSAPAKGVBELESCEVYQSLK 1564
 Db 1505 MSLUSLNLEGAVSANOCSVDEVFCSSLQEEENLTKTPSAPAKGVBELESCEVYQSLK 1564
 Db 1505 MSLUSLNLEGAVSANOCSVDEVFCSSLQEEENLTKTPSAPAKGVBELESCEVYQSLK 1564
 Qy 410 -QEDNSKNUSLNQFLPLRILLESKPYRPTDVLVLEEHKEIAIJKQELRFQFVSLST 468
 Db 410 -QEDNSKNUSLNQFLPLRILLESKPYRPTDVLVLEEHKEIAIJKQELRFQFVSLST 468
 Db 410 -QEDNSKNUSLNQFLPLRILLESKPYRPTDVLVLEEHKEIAIJKQELRFQFVSLST 468
 Qy 1565 LEEBKSOQI-MKNGQIYKQELRFQFVSLST 468
 Db 1565 LEEBKSOQI-MKNGQIYKQELRFQFVSLST 468
 Db 1565 LEEBKSOQI-MKNGQIYKQELRFQFVSLST 468
 Qy 469 SGKXQFLADSITMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLJG 528
 Db 469 SGKXQFLADSITMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLJG 528
 Db 469 SGKXQFLADSITMSLNHPLAPVRLAMPHLKKMITSKEGYDIFIKEAVLJG 528
 1617 LEMSKLAAEKQKOTQFQSLLEVARLQL-----QGDL-----SRSLGJ 1657

Qy 529 DNIDVWLSA5A5AFETKEHFSSEVT-----ISNLNLFRAEISKNGEWYEVLKTAAD 581
 Db 1658 DTEDAIQGRNNSCDISKEH-TSETERTPKDVKHQICDQDQDNL---LDIEKET 1711
 Qy 582 IILKE--EISSENDOLSNQVNUCLPFVVIINDDTSAEMKIAIYISKSGICSLHLL-LR 638
 Db 1712 GALKPTGECSGEQSPDT-----YEPPOEDKTQGSSSECIS-ELSFSGPNALVMDFL 1762
 Qy 639 GWEAEALENV--IKSPKPGKU-----IGVANQKMFELAD-----NINQDPPSSMUKM- 683
 Db 1823 ACIELKIVGKLEKNSDLSBKELEYFSCDHQELGRVETSEBGLNSLEMHADKSS 1882
 Db 1763 GNOEDIHNQLQKVKETSNENLRLHVIEDRDRVKVSESLNENKELDSKLUHQEVQMLKIE 1822
 Qy 684 ---VEDLISGBEEFSNPNUKOKVTF---HVLISVLSVCCSSLK--ETHFPAIRV- 729
 Db 777 STORVAV---EDSVFLVFSLSKKFTYALKAPKSPFKGDI-----WNNEBOLKEDSRYL 826
 Db 1928 OTEKUCLBKDNENKQKVKIVCIEBELSVUTSERNQLGELDTMSKKTALDQDLSERKET 1987
 Db 1988 Q-----ELSHOSECILCIVAOEAVKEKTE-----LLQTLSSDVSELLKDTH 2031
 Qy 827 HLLIGLUFEMMINGADAVHFRVLMKPLIKVHEDVOLFKFCCSVLWYGSISNPNCSVK 886
 Db 887 TVLQTOALIYVGAMLSQSKQCKHOLA-----SISSP 918
 Db 2032 1QEKQUSLEKUSQSOAISLTKCDELNGIAQNLNEKEKESLSOARLSSESBYEKUNSA 2091
 Qy 919 VVTSLI-----INJGSPVKEVR--RAAIQCLQALSGVASPFYLIDHLLISKAETSDA 970
 Db 2092 LEALALVEKGERALRUSSTQEQVHQLRGIEKLVRVREADEKQK--HIAEKLKEREREN 2148
 Qy 971 AVYDOLATLFEELBOKKU-KSHOKU-----SETKNLSCVSCPSYAKD 1018
 Db 2149 ---DSLKDVKVENLERBLONBSEENOBLVILDAENSKAETVLTQTEEMARSLSKVFIELDL 2204
 Qy 1019 M-----KVLOGVNGEN-VISQOLPMAEOLBKEKIQEPTAV-LKDEM-----VTLH 1062
 Db 2205 VTLRSBRENUTKQIKBQGQISLELDKULSSFRSLLE--EKOAEQIYKEEKTAVMLON 2262
 Qy 1063 TLGKNEPFSVSLNED-----PKSDIFIKVHTKELYAGMPTIQITALEKIKTRPFA 1116
 Db 2263 OLKELNEAVALALCGPOEIMKATEOSLDPPRIBEEHOR-----NSIEKLARLEA 2311
 Qy 1117 AIDSERKQOKLARMFEDLVLVNCNSQHQAVSVSSVKGIS-----VNAEQVIELEPPD 1169
 Db 2312 ---DERKQOLCQLQIKE-----SEHHADLKGRYNTLEBLERLARTNQEHALBRAENSK 2362
 Qy 1170 -----KAKPLGTVOQRROMQKKSQDLSRQEVGGSYWORTVILLELIOQKKKLSP 1223
 Db 2363 GEVETIKAKEGMTSLSRGEI-----DVUTRS-----EKENITNEQKEQRISEL 2410
 Db 1224 QIOLVPTFLNLSRCLEPLPBOBQNMWYTKQILSCHLNLCKLSPDGKPKD--TLDDE 1281
 Qy 2411 EINNSFENTI---LOKEQEVKOMKSTAMEMLOTOIKRKLNERVAALKINDQEACK 2466
 Db 1282 KENVELIVQVIRLE-----MPQTHHALLJLGTAGF-----PDVHLNI 1323
 Qy 2527 KNOQDQDQVLSKLSQVEGHQMLKEONLIRNLVTEBKQIYQSKNLSQDPTFVQ 2586
 Db 2467 EONLSSQVECBLEKQQLQGQDDEAKNNYVLUQSSVNGLQOVEDQKQKLEKKDEBISRL 2526
 Qy 1324 NSIFTPMGANNMRDIT-----YSFQVINKVNMVP-ALIOSDSG--DSEV- 1368
 Db 2587 SYKONLNELELITKDMKSFVEVKVKONTAKTELQREMHEM-MAQKTAELQBSLGEKRLA 2646
 Qy 1413 WILLIFLFCOYVKTWLAAYGEKAILEADTEFWFSVCC----- 1452

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Run on:	Copyright (c) 1993 - 2006 Biocceleration Ltd.					
	June 29, 2006, 00:41:09 : (without alignments)					
	search time 144.903 Seconds					
	(6765.010 Million cell updates/sec)					
Title:	US-09-603-665-5					
Perfect score:	10803					
Sequence:	1 MTSIAQQLQLRILAPQSDASL..... CQKTRIQQLETVLGPQLSYF 2144					
Scoring table:	BLOSUM62					
Gapop:	10.0 , Gapext: 0.5					
Searched:	2589679 seqs, 457216429 residues					
Total number of hits satisfying chosen parameters:	2589679					
Minimum DB seq length:	0					
Maximum DB seq length:	20000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	A_Geneseq_8:*					
	1: geneseqp1980s:*					
	2: geneseqp1990s:*					
	3: geneseqp2000s:*					
	4: geneseqp2001s:*					
	5: geneseqp2002s:*					
	6: geneseqp2003as:*					
	7: geneseqp2003bs:*					
	8: geneseqp2004as:*					
	9: geneseqp2005s:*					
	10: geneseqp2006s:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
Result No.	Score	% Match	Length	DB ID	Description	ALIGNMENTS
1	10799	99.9	2144	4 RAB85029	Ab85029 Protein e	RESULT 1
2	10799	99.9	2144	8 ADQ85800	Adq85800 Antagonis	ID AAB85029
3	10791	99.9	2144	9 AEE02859	Aee02859 Human S-1	ID AAB85029;
4	10782	99.8	2144	8 AD334902	Ad334902 Human aut	XX DT 06-AUG-2001 (first entry)
5	10222	94.6	2044	8 AD334907	Ad334907 Human aut	XX DR Protein encoded by BAP28 cDNA consisting of exons 1 to 45.
6	9853	91.2	2036	8 AD334903	Ad334903 Human aut	XX FT BAP28; prostate; tumour; cancer; diagnostic; genetic analysis.
7	9853	91.2	2036	8 AD334904	Ad334904 Human aut	XX OS Homo sapiens.
8	9853	91.2	2036	8 ADG15232	Adg15232 Novel hum	XX FT Misc-difference 1967
9	7756.5	71.8	1569	4 ADQ66400	Adq66400 Novel hum	FT FT Misc-difference 2017
10	6124.5	56.7	1229	8 ADQ69152	Adq69152 Novel hum	FT FT Misc-difference 2017
11	5026.5	46.5	1149	7 ADP08012	Adp08012 Novel pro	FT FT Misc-difference 2017
12	5026.5	46.5	1149	9 ADU40382	Adu40382 Novel hum	FT FT Misc-difference 2017
13	4506	41.7	897	8 ADQ96220	Adq96220 T cell ac	FT FT Misc-difference 2017
14	4498	41.6	897	8 ADQ96218	Adq96218 T cell ac	FT FT Misc-difference 2017
15	4494	41.6	897	8 ADQ96152	Adq96152 T cell ac	FT FT Misc-difference 2017
16	3694	34.2	734	7 ADM04615	Adm04615 Human pro	FT FT Misc-difference 2017
17	3694	34.2	734	9 ABC87545	Aec87545 Human cDN	FT FT Misc-difference 2017
18	3102	62.4	1149	9 AEE02884	Aee02884 Protein I	FT FT Misc-difference 2017
19	2585	23.9	515	2 ADW54099	Adw54099 Homo sapi	FT FT Misc-difference 2017
20	2061	19.1	408	8 AD334906	Ad334906 Human aut	FT FT Misc-difference 2017
21	2051.5	19.0	408	4 ABB65242	Abb65242 Drosophi	FT FT Misc-difference 2017
22	2051.5	19.0	2096	8 ADQ89606	Adq89606 Antagonis	FT FT Misc-difference 2017
23	1779	16.5	349	8 ADP24166	Adp24166 PRO polyp	FT FT Misc-difference 2017

The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3', and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. BAP28 polynucleotides and polypeptides have been found to be over expressed in prostate tumor cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g., by polymerase chain reaction (PCR)) to diagnose patients suffering from or susceptible to prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers for the BAP28 gene are useful in genetic analysis. The present sequence represents a protein encoded by a first cDNA sequence of the BAP28 gene consisting of the exons 1 to 45

Best Local Similarity	Locid	Nov.	Loc	Length	Matches
100.0%	1	0	0	0	Mismatches
99.9%	1	0	0	0	MSLAQQQLRPLFOSDASLISRSDEVASLIFDPKKAATIDRTAFAIGCTGLEELIGIDP 60
99.9%	1	0	0	0	MTSLAQQLRPLFOSDASLISRSDEVASLIFDPKKAATIDRTAFAIGCTGLEELIGIDP 60
99.9%	61	0	0	0	SFEQFPEAPLFSOLAKTLERSVOTKAVNKVOLDENTSLSFLHILSPYUPLKPAQKCLEWLHR 120
99.9%	61	0	0	0	SFEQFPEAPLFSOLAKTLERSVOTKAVNKVOLDENTSLSFLHILSPYUPLKPAQKCLEWLHR 120
99.9%	121	0	0	0	FTHILYNQPSLIACVLPYHETRIFVUOLKINNSKRFREWLLVYKQSEVPLAKGTLIT 180
99.9%	121	0	0	0	FTHILYNQPSLIACVLPYHETRIFVUOLKINNSKRFREWLLVYKQSEVPLAKGTLIT 180
99.9%	181	0	0	0	HCYKDLGFMDFICSLVTKSYKVAEYPPGSAQRLVLAFYASTVUSALVAEDSDNII 240
99.9%	181	0	0	0	HCYKDLGFMDFICSLVTKSYKVAEYPPGSAQRLVLAFYASTVUSALVAEDSDNII 240
99.9%	241	0	0	0	KLFPYIQKGLKSSLPDYRAATYMIICQISQVKMFTFVNLASQIKTJKLPSLKD 300
99.9%	241	0	0	0	KLFPYIQKGLKSSLPDYRAATYMIICQISQVKMFTFVNLASQIKTJKLPSLKD 300
99.9%	301	0	0	0	LSCLIVLVLQROKPSLIGKKEPPHLGNNPDLITLHGISETYDVSPLRMLPHVSIH 360
99.9%	301	0	0	0	LSCLIVLVLQROKPSLIGKKEPPHLGNNPDLITLHGISETYDVSPLRMLPHVSIH 360
99.9%	351	0	0	0	HVTGBETEGMDQYKRRHBAILTKISLKNLDLHLASLIFEEYISSSQEBEMSNKVL 420
99.9%	351	0	0	0	HVTGBETEGMDQYKRRHBAILTKISLKNLDLHLASLIFEEYISSSQEBEMSNKVL 420
99.9%	421	0	0	0	LNEOFLPLRLJESKPYRTDVLVIEBHLKIAIDLKKQELHQFUSLSTSCKYQFLADSD 480
99.9%	421	0	0	0	LNEOFLPLRLJESKPYRTDVLVIEBHLKIAIDLKKQELHQFUSLSTSCKYQFLADSD 480
99.9%	541	0	0	0	TSMLSLNHLAPVIRILAMHHLKCKMTKTSKEGVDSFSTKEAVLARLGDDNDVVIISA 540
99.9%	541	0	0	0	TSMLSLNHLAPVIRILAMHHLKCKMTKTSKEGVDSFSTKEAVLARLGDDNDVVIISA 540
99.9%	481	0	0	0	TSMLSLNHLAPVIRILAMHHLKCKMTKTSKEGVDSFSTKEAVLARLGDDNDVVIISA 540
99.9%	541	0	0	0	FELFKEHSSSEVTISNLNLFORAELSKGEGWYETLKIAIDLKEEISSENDOLSNQV 600
99.9%	541	0	0	0	FELFKEHSSSEVTISNLNLFORAELSKGEGWYETLKIAIDLKEEISSENDOLSNQV 600
99.9%	601	0	0	0	VCLIPFVWINDDESAEMKAIYLSKGCSSLHPLRIGBEALENVISTKPGKLGVA 660
99.9%	601	0	0	0	VCLIPFVWINDDESAEMKAIYLSKGCSSLHPLRIGBEALENVISTKPGKLGVA 660
99.9%	721	0	0	0	THEFFPAIRYFVSLQKIKKLESVITAVEPSEWBELMLORGIPWELWVYVEELNSTOR 780
99.9%	651	0	0	0	NOKMTELLADNNINGDPSSNLKMKVEDLISVGEBEEFNLKOKYTFVVLISLVLSCSSLKE 720
99.9%	651	0	0	0	NOKMTELLADNNINGDPSSNLKMKVEDLISVGEBEEFNLKOKYTFVVLISLVLSCSSLKE 720
99.9%	721	0	0	0	THFFPAIRYFVSLQKIKKLESVITAVEPSEWBELMLDRGIPWELWVYVEELNSTQR 780
99.9%	781	0	0	0	VAVEDSVFLVSLKRFIYALKAKPSFPKGIDWNBOLKEDSDYVHLHLIGFEMUNGLA 840

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GenCore version 5.1.9

OM protein - protein search, using sw model
Run on: June 29, 2006, 00:42:00 ; Search time 51.7106 Seconds
(without alignments)
3989.395 Million cell updates/sec

Title: US-09-603-665-5

Perfect score: 1003

Sequence: 1 MTLAQLQRLALPQSDASL.....COKTIOQLETVLGEPIQSYF 2144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries
Database : PIR_801:
1: piri:
2: pi2:
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4: pir4:
5: piri:
6: pi2:
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37: piri:
38: piri:
39: piri:
40: piri:
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43: piri:
44: piri:
45: piri:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	990.5	9.2	1649	2	T3993B	hypothetical protein SPBC23E6.04C - fission yeast (<i>Schizosaccharomyces pombe</i>)
2	956	8.8	1769	2	S5337B	hypothetical protein
3	857	7.9	1650	2	T27864	probable membrane protein
4	3175	2.9	1650	2	T37919	hypothetical protein
5	279	2.6	2672	2	A48126	GCN4 homolog - fission yeast
6	272.5	2.5	2954	2	T14156	translation activator
7	268.5	2.5	2663	1	S28261	kinesin-related protein
8	268.5	2.5	2819	2	A90551	centromere protein
9	261.5	2.4	1727	2	T50073	conserved hypothetical protein
10	250	2.4	4385	2	T29042	myosin-like coiled-coil protein
11	257	2.4	2297	2	AB2494	hypothetical protein
12	256.5	2.4	1837	2	T41023	probable nuclear protein
13	255.5	2.4	3433	1	S28381	utrophin - human
14	254.5	2.4	2895	2	H85362	hypothetical protein
15	252	2.3	3655	2	T38084	TRAP-like protein
16	249.5	2.3	3187	2	JC3817	364K Golgi complex
17	249	2.3	2401	2	T28675	hypothetical protein
18	247	2.3	2493	2	T40540	hypothetical protein
19	245	2.3	2433	2	T41933	large tegument protein
20	244.5	2.3	2514	2	T37320	ataxia telangiecta
21	244	2.3	2110	2	H96803	unknown protein T5
22	243	2.3	2110	2	T28677	hypothetical protein
23	242	2.2	1964	2	A59282	nonmuscle myosin I
24	238	2.2	1957	2	T38077	hypothetical coiled-coil protein
25	236.5	2.2	1830	2	E82909	conserved hypothetical protein
26	235.5	2.2	2471	2	T42977	large tegument protein
27	235	2.2	1919	2	T40032	hypothetical protein
28	234	2.2	3795	2	T00831	hypothetical protein
29	232.5	2.2	2166	2	G70163	hypothetical protein

ALIGNMENTS

Qy	2	TSLAQQLQRLALPQSDASLRSDEV--ISLFLDPKEAATIDRATAFAIGCTGRELGI	RESULT 1
Db	3	SSLOQQLQKNT--QSN-NVILKINKIRRAPSLLVDPKVAADMDDLEBIVYTAWSGFHELAVH	T3993B
Qy	59	DPSFBQFPEARFLPSOLAKTIVRSVQTKAVNQKLDENISLFLHILSPYFLLKPAQKCLEWLI	58
Db	59	EPRLVYFEKLIGLQPSQVQDPRVLLNTRENKEKIDLCVQQLRLLAPPFTEKNAKYLEWLI	118
Qy	119	HRFHFLYHMQDLSLACIACVLPYHETRIFRVTRVYIQLKINNSKHWFWFLPLPVQSGVPLAKTL	178
Db	119	RRFSTIHEYVSDFLISFLSPFLPHDPFFARLIGCSK-PKSRLPLFENAIKMP-VLISRADI	176
Qy	179	I THCYKDGLGMDTCSLVTKS VKYFAEYVGSSAQRLVLA FAYSTIVSVAEDVSDN-	237
Db	177	WHAISRDRKEFFAMFAQFVQNTAESHNMYP-----ELARFWAGTMEVIAWHSSNEDP	229
Qy	238	-I IAKLPPVYQKGK- S SLPD YRAATM I CQI S V K U T M E F V N S L A S Q I K L T K I	293
Db	230	NVLLDPRFLRVS YAVSYVSS- DFOIAGM L L S S I A A S L P L S P I I P P L V A I D R L S F	287
Qy	294	PSLKGDLGSLCILVIL-----Q R Q K P E S L G -----	317
Db	288	-DNIKPA L I C V G H I L Q F C S F E F H E Q L E K L E S G A S S I L E L S Q E H R D F F Y W V S L	346
Qy	318	-----KKPFPHLCNVPDLT I L H G I S T E D V S P I L Y R M P L H V V S I I H H V G E E T G M D	372
Db	347	I K S R Q K D K K R L I S L D - T S I S Q I R V T H Q K A F L L S V I P -----W N Q P F K A L -	392
Qy	373	Q I Y K R H L E A I I T K I S L K N N D H L L A S L L F E E Y I S S Q E B M D S N K V S L N E Q F L P L I R L L	432

Db	999	HDFCLTLVQSFSSVADRIGSINQCSRFLCKLSLEQNSNSNGKAVSLIKDEL-----MD	
393	OSYRILDSVIOPERKEGKLDNLINTL-----ODKKKSSTFSKKOREVL-----	436	
Qy	ESKYPRTLDVUVEEHEKJEAIDJKKQELFHOFVLSLSTSGGKVQFLADSSTSMLSLNHPA	492	
433	-LKKSEIDSQPSFEOCLAYADSA-----ADLSVYFISL-----	470	
Db	437	-----	
Qy	493	PVRILAMNHKKMITSKEGVDFEIKEAVIARLGGDDNIDVLSAISAFETFKERFSEV	552
Db	471	-----	
Qy	553	TISNLNLNLFORAEKSNKEGEWEYVUJKIADILIKEELSENDOISNOVVCULPPVV--IN	610
Db	493	ILILSLRL-----RKTIEENKODVQIT--LPVVLISLQ	524
Qy	611	NUDTTESEMKAIAVLKSGKICSLHPLLRGWEBALEENVIKSTKPGKLGIVANQKMBELLAD	670
Db	548	NL-----EESIYGMDDN-----	562
Qy	525	SKDTEVRSRALNLT-----	547
Db	731	SILQKKKKLESVITAVEIPSEWHIELMDRGPVEWAHYVEELNSTORVAVESVFLV	790
Qy	563	563-----KJNRLWLSPT-----KVICSDLILRSSEIGL-----	596
Db	791	FSIKKFYIYALKAPSKPSFKPGDIWNNEPQLKEDSRDYYLHLLIGLFEMMLNGADAVHFRVLMK	850
Qy	620	SFLSH-----	633
Db	597	SYIPELFTEKKPNASK-----	619
Qy	851	LFIKVHEDVQFLKFCSVLWVYSSLNSNPLNCVKVLUQTOALYVGAMLSQKQCKH	910
Db	911	QLASISSPPVITSLNLINGLSPVKEVRRAIQCQALSGVASPFLIDHLISKAEITSDA	970
Db	634	-----VRLVILLEIJTRVHG-----	651
Qy	971	AVVIDQIATLFEELFQERKEKLKSHQKUSCETBLKQNLSCVYSCPSYIADQMLKVQGVNGEMV	1030
Db	652	-----AKMQLLPRLEQSEFNS-BKFTVSKVKEBEALVNCFNHTS--FTSISLSPFNNIV	704
Qy	1031	LSQOLPMAEQLERKIKOKEPTAVLKLDEAMVHLITLGKYNFESVSLNLNEPDPSLIDFIAKVH	1090
Db	705	1SQAII--CRRIVE--IOS-----HL-----KDPQRL-EFVAKI	733
Qy	1091	TIKELIYAGMPTIQITALEKIKPFFAISDERVKQKULMFDLJNCKNSHCAQVSS	1150
Db	734	SODE---OPHYVVDVDSIKP-----	755
Qy	1151	FRGGSIVNAEQVRIELEPPDKAKPLGTWQOKRQRMQOKKSODLESVQEVGGSYWORTLI	1210
Db	755	FR-----KLGSTVKPKPATKRKIDS--HIFQDVRQTRI	794
Qy	1211	LEUHQKKKLRSPOOLVPTLNLSRCLEPLPQBOGNNYETKQMLLCLNT-----CQK	1265
Db	795	LELETQKMAASIPKLAASP--LFEVLNVI--ALKEDIVSSNLYLQLLGILYEMIGASPIE	852
Qy	1266	LSPDGKIPKPDILDEEKENVELVOCIRLSEMPOTHHALLIGTVAGIFPKVLNIMS	1325
Db	853	1326-----SIRIDTUVGICRSTNNPQIQNKALLVSLANAAPEAVLHGMP	899
Qy	900	ITFFMGANVMRADDITYSQVINKTQVIMPAIQ--SDSGDSIEVSNEVEWKITSVF	1383
Db	1384	1384 VDALLPHVPEHRRILPILVOLVDTGAEKLWILLLFEQVTKTVAAGYBKDAILEAD	1443
Qy	948	VNAFPHTPQHRRJRLYRLVQITGSNRELWSVLI--QFAEMMLA----KSTNNUA	998
Qy	1444	TERWPSVCEFSVHQIQISMLNTIQYLLKPEEK--BETIPKAVSNKESOBEMQVFN	1501

RESULT 2

553378 probable membrane protein YJH109c - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: hypothetical protein J0808
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 05-May-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: SS3378, SS5887, SS7359
 R;Rasmussen, S.W.
 submitted to the EMBL Data Library, February 1995
 A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and C
 A;Reference number: S53376
 A;Accession: SS3378
 A;Molecule type: DNA
 A;Residues: 1-1769 <RAS>
 A;Cross-references: UNIPROT:P42945, UNIPARC:UPI000052F40; EMBL:X85021; NID:9728698; PID:
 R;Rasmussen, S.W.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56876
 A;Accession: S56887
 A;Molecule type: DNA
 A;Residues: 1-1769 <RAW>
 A;Cross-references: UNIPARC:UPI000052F40; EMBL:249384; NID:9108292; PID:9108293; MIPS:

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 00:41:34 ; Search time 219.344 Seconds
(without alignments)
9041.668 Million cell updates/sec

Title: US-09-603-665-5
Perfect score: 10803
Sequence: 1 MTSIAQQLQLPQDSL.....CQKTIQOLETVLGEPLQSYF 2144

Scoring table: BL2S6M2
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database : UniProt 7.2;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

SUMMARIES

ALIGNMENTS

DESCRIPTIONS

Result No.	Score	Query	Match length	DB ID	Description
1	10791	99.9	2144	1	HEATR_HUMAN
2	10342.5	95.7	2063	2	Q5T3Q7_HUMAN
3	5807.5	53.8	2159	2	Q7SY48_BRACHYDANIO
4	5562	51.5	1106	2	Q6P191_HUMAN
5	4944	45.8	2288	2	Q4T723_TETRAODON
6	4891	45.3	1180	2	Q3UNW7_MOUSE
7	4729	43.8	958	1	HEATR_MACRA
8	4516	41.8	1090	2	Q3TNEL_MOUSE
9	4494	41.6	897	2	Q8N717_HUMAN
10	4072	37.7	984	2	Q3TMK0_MOUSE
11	3935.5	36.4	1336	2	Q7T152_BRARE
12	3669.5	34.0	1278	2	Q3V1X6_MOUSE
13	3315.5	30.7	743	2	Q8BLJ4_MOUSE
14	3099	28.7	733	2	Q3T9I0_MOUSE
15	3095	28.6	733	2	Q7PWD5_ANOGA
16	2156.5	20.0	2104	2	Q7PWF6_ANOGA
17	2051.5	19.0	2096	1	HEATR_DROME
18	2001.5	19.0	2096	2	Q6AW50_DROME
19	1926	17.8	408	2	Q8CC75_MOUSE
20	1779	16.5	349	2	Q96E55_HUMAN
21	1682	15.6	349	2	Q8VCKL_MOUSE
22	1462.5	13.5	1690	2	Q8T9E7_DROME
23	1415	13.1	2237	2	Q54ML4_DICDI
24	1252	11.6	2122	2	Q5CAF8_ORYSA
25	1194.5	11.1	1830	1	HEATR_ARATH
26	1142	10.6	2021	2	Q5KBQ7_CRYNE
27	1134	10.5	2021	2	Q5SNB7_CRYNE
28	1127.5	10.4	1801	2	Q5B1X5_EMENI
29	1127	10.4	1857	2	Q6BX05_DEBHA
30	1104	10.2	1802	2	Q2ULC6_ASPO
31	10.1	10.1	1798	2	Q4WL19_ASPPU

32	1056.5	9.8	1818	2	Q59ZX6_CANAL	059ZX6_candida alb
33	1049.5	9.7	2251	2	Q4P937_USTMIA	04P937_ustilago ma
34	1030.5	9.5	1788	2	Q7R2MB_NEUCRA	07r2mb_neurospora
35	1006.5	9.3	1770	2	Q6FT93_CANGA	06ft93_candida gla
36	1003.5	9.3	1774	2	Q6CJ57_KLUUA	06cj57_kluveromyces
37	990.5	9.2	1649	1	Y4C4_SCHPO	060179_schizosaccharomyces
38	965	8.9	1806	2	Q41656_GIBRE	041656_gibberella
39	956	8.8	1769	1	U7P10_YEAST	P42945_saccharomyces
40	950.5	8.8	1774	2	Q754J8_ASAGO	Q75418_aspergillus
41	903	8.4	1635	2	Q6C457_YARIT	Q6C457_yarrowia li
42	870.5	8.1	1660	2	Q61Y68_CAEER	Q61Y68_candida easter
43	857	7.9	1650	1	HEATR_CAEEL	Q23195_caenorhabditis
44	852	7.9	168	2	Q2K1F9_BOVIN	Q2K1F9_bos taurus
45	773	7.2	2034	2	Q519S9_ENTHI	Q519S9_entamoeba h

Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., RT
 "Complete sequencing and characterization of 21,243 full-length human RT
 cDNAs"; RT
 Nat. Genet. 36:40-45 (2004). RL
 [4] IDENTIFICATION BY MASS SPECTROMETRY, AND SUBCELLULAR LOCATION. RL
 RX MEDLINE=22317277; PubMed=12429849; DOI=10.1093/obc/ob2-05-0271; RL
 RA Scherl A., Goutte Y., Deon C., Caille A., Kindbeiter K., Sanchez J.-C., Greco A., Hochstrasser D.F., Diaz J.-J., "Functional proteomic analysis of human nucleolus. "; Mol. Biol. Cell 13:4100-4109 (2002). RL
 CC -i- INTERACTION: CC
 CC Q8B87; XRN1; NBEXP1; IntAct-EBI-373098; EBI-372406; CC
 CC -i- SUBCELLULAR LOCATION: Nuclear; nucleolar. CC
 CC -i- SIMILARITY: Belongs to the HEATR1 family. CC
 CC -i- SIMILARITY: Contains 1 HEAT repeat. CC
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 Distributed under the Creative Commons Attribution-NonDerivs License. CC
 CC
 DR AX067150; CAC26776.1; -; Unassigned DNA. DR
 EMBL; AX067150; CAC26776.1; -; Unassigned DNA. DR
 DR EMBL; AX067150; CAC26776.1; -; Unassigned DNA. DR
 DR EMBL; AK001221; BAA91544.1; ALT_INIT; mRNA. DR
 DR INACT; Q9H83; -; SWISS-2DPAGE; Q9H83; HUMAN. DR
 DR Ensembl; ENSG00000119255; Homo sapiens. DR
 DR HGNC; 25517; HEAT1. DR
 GO; GO:0005515; F:protein binding; IPI. DR
 DR InterPro; IPR012954; BP28_C. DR
 DR InterPro; IPR00357; HEAT. DR
 Pfam; PF08146; BP28CT; 1. DR
 PRM; PF02915; HEAT; 4; HEAT REPEAT; FALSE_NEG. PRM
 PROSITE; PS0077; HEAT REPEAT; FALSE_NEG. PROSITE
 KW Nuclear protein; polymorphism. KW
 FT CHAIN 1 2144 HEAT repeat-containing protein 1. FT
 PT REPEAT 2106 2142 /FTId=PRO_0000186201. PT
 FT VARIANT 1694 1694 HEAT. FT
 FT VARIANT 1854 1854 N -> S. FT
 FT VARIANT 1967 1967 /FTId=VAR_010939. FT
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 FT VARIANT 1967 1967 /FTId=VAR_010941. FT
 FT VARIANT 2017 2017 B -> G. FT
 FT CONFLICT 348 348 /FTId=VAR_010942. FT
 FT CONFLICT 607 607 H -> R (in Ref. 1). FT
 SQ SEQUENCE 2144 AA; 242370 MW; 7590821749A9F39D CRC64; SQ
 Query Match 99.9%; Score 10791; DB 1; Length 2144; DB
 Best Local Similarity 99.7%; Pred. No. 0; DB
 Matches 2138; Conservative 1; Mismatches 5; Indels 0; Gaps 0; DB
 Qy 1 MTSIAQQLRQLDQSDASLRLRDEVASLIFDPKSAATIDRTAAGCTGLELLGIDP 60 Qy
 1 MTSIAQQLRQLDQSDASLRLRDEVASLIFDPKSAATIDRTAAGCTGLELLGIDP 60 Qy
 61 SFEGEPEAPLPSQALKLERSVOTKAVNKLQDENISLFLIHSPIYLLKPAOKCLEWLIHR 120 Qy
 61 SFEGEPEAPLPSQALKLERSVOTKAVNKLQDENISLFLIHSPIYLLKPAOKCLEWLIHR 120 Qy
 121 FTHILYNODSLIAVLPYHETRIVFVOLIKINNSKRNFWLILPKQSGVPLAKGLT 180 Qy
 121 FTHILYNODSLIAVLPYHETRIVFVOLIKINNSKRNFWLILPKQSGVPLAKGLT 180 Qy
 181 HCYVQDGLGFDIFCISLVTKSIVYFAYPGSSAQRLVLAFASTVSALVAEDVSDNIIA 240 Qy
 181 HCYVQDGLGFDIFCISLVTKSIVYFAYPGSSAQRLVLAFASTVSALVAEDVSDNIIA 240 Qy
 181 HCYVQDGLGFDIFCISLVTKSIVYFAYPGSSAQRLVLAFASTVSALVAEDVSDNIIA 240 Qy
 241 KLFPIYIOKGKSSPDYRAATYMICQISQYKMENTFVNSLASQIKTUKTPSLIKDG 300 Qy
 241 KLFPIYIOKGKSSPDYRAATYMICQISQYKMENTFVNSLASQIKTUKTPSLIKDG 300 Qy
 241 KLFPIYIOKGKSSPDYRAATYMICQISQYKMENTFVNSLASQIKTUKTPSLIKDG 300 Qy
 301 LSCLTVLQLRKPSLGKPFPHCNVPLILHGISETVSPPLRMLPHLVVSH 360 Qy
 301 LSCLIVLQLRQKPSLGKPFPHCNVPLILHGISETVSPPLRMLPHLVVSH 360 Qy
 361 HVTGEETEGMCGQIYKHLBAILTKSISLKNNDLHLASLRFYIYSSQERMDNSKVSL 420 Qy
 361 HVTGEETEGMCGQIYKHLBAILTKSISLKNNDLHLASLRFYIYSSQERMDNSKVSL 420 Qy
 421 LNEQFPLRILLESKPRTDVLEELHLKEADLKKOELFQFVSLSTGGYQFLSD 480 Qy
 421 LNEQFPLRILLESKPRTDVLEELHLKEADLKKOELFQFVSLSTGGYQFLSD 480 Qy
 481 TSMLMSLNLHPLAPVRLAMNLKMKMTSKEGVDESFIKEAVLRLGDDNDIVVLSAISA 540 Qy
 481 TSMLMSLNLHPLAPVRLAMNLKMKMTSKEGVDESFIKEAVLRLGDDNDIVVLSAISA 540 Qy
 541 FEIKERFSEVTISNLNLTQAEISKNGEYEVLTIAADILKEETISENDOLSNQVV 600 Qy
 541 FEIKERFSEVTISNLNLTQAEISKNGEYEVLTIAADILKEETISENDOLSNQVV 600 Qy
 601 VCLLPFWVNNDDTESAEMKIAIYLKSGISLHPLRGWEALENTIKSTPKGLIGV 660 Qy
 601 VCLLPFWVNNDDTESAEMKIAIYLKSGISLHPLRGWEALENTIKSTPKGLIGV 660 Qy
 661 NOKMIELLADANLNGPDSMLKNDVLSGEEBESNLKQVYTFHVLISVLYSCSSLKE 720 Qy
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 721 THFPFAIRVFSLQQKKLLESVITAVEIPSPRWHIELMDRGIPVEMJAHYBELLNSTR 780 Qy
 721 THFPFAIRVFSLQQKKLLESVITAVEIPSPRWHIELMDRGIPVEMJAHYBELLNSTR 780 Qy
 780 VAVEDSVFLVFSLLKKFIYALKAKPSFFKGDIWNPEQLEKEDSRDYLHLIGFEMMLNGA 840 Qy
 781 VAVEDSVFLVFSLLKKFIYALKAKPSFFKGDIWNPEQLEKEDSRDYLHLIGFEMMLNGA 840 Qy
 841 DAVHFRTIMKLFKIVLEDVQFLKQCSVLMYGSISNPNCVSKVTLQTOLYVGCA 900 Qy
 841 DAVHFRTIMKLFKIVLEDVQFLKQCSVLMYGSISNPNCVSKVTLQTOLYVGCA 900 Qy
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 901 LSSQKTOCKHOLASISSPVVTLINGSPVKEVRRAIQCQIQLASGVASPEFLIDII 960 Qy
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 961 SKAETTSDDAAVVIQDIALEELQREKKLKHQKUSSETKULSCYSCPSYIAKDLMK 1020 Qy
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 1021 VLGQVNGEMVWSQQLPNAEQLKIQKEPTAVLKDANVHLJLIGKNEFNSVSLNEDPK 1080 Qy
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 1081 SIDIFIAVHTKELYAGMPTQITALBKTPPKFAAISDEKVKQKLMLPDLVNCN 1140 Qy
 1081 SIDIFIAVHTKELYAGMPTQITALBKTPPKFAAISDEKVKQKLMLPDLVNCN 1140 Qy
 1141 SHCAQTVSSVEKGISYNAEQVIELEPPDKAQLPGLWVQKQKQMKQKQKQKQDLSVQEVG 1200 Qy
 1141 SHCAQTVSSVEKGISYNAEQVIELEPPDKAQLPGLWVQKQKQKQKQDLSVQEVG 1200 Qy
 1201 GSYWQRTILLELQKQKLRSPQIYPLTFLNLSRCLEPLQEQGMYETKQILSLC 1260 Qy
 1261 NICQKUSPDKGKIPKDILDEBEKVENELJVQCLRCIASEPQTHHALLJLIGTVAGIFPDKWL 1320 Qy
 1261 NICQKUSPDKGKIPKDILDEBEKVENELJVQCLRCIASEPQTHHALLJLIGTVAGIFPDKWL 1320 Qy
 1261 NICQKUSPDKGKIPKDILDEBEKVENELJVQCLRCIASEPQTHHALLJLIGTVAGIFPDKWL 1320 Qy
 1321 HNIMSIPTFMGANVMLRDDTSFQVINKTKVAPLTDSDGDSIEVSRNVEIVVKII 1380 Qy
 1321 HNIMSIPTFMGANVMLRDDTSFQVINKTKVAPLTDSDGDSIEVSRNVEIVVKII 1380 Qy
 1381 SVEFDALPHVPHRRFLFVLOVLDLQRAKEFVWILLFILFEOVTKVLAAYGEKDQI 1440 Qy

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GenCore version 5.1.9

Run on: June 29, 2006, 00:46:09 ; Search time 37.5044 Seconds

(without alignments)

5003.834 Million cell updates/sec

OM protein - protein search, using sw model

Title:

US-09-603-665-5

Perfect score:

10003

Sequence:

1 MTSLAQOLRILALPOSDSL.....CQKTIQOLETVLGERPLQSYF 2144

Scoring table:

BLOSUM62

Gapop 1.0 , Gapext 0.5

Searched:

650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:

650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

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QY 1758 L---SALAALQKVVENTLPHFISPVYEGILSOVIRHKBITSMSA----- 1799
 Db 341 LLQGSVIVLVLSCYKKIPAFMSTLBAVLTLSLDLIDNHRSSVLDLIVDHMDLAQL 400
 QY 1800 -SOAIVRLTSLKKTATTLPAPRVLPAIKKVKQFLEKWNKHMGPMSILOEHGQXMKKE 1858
 Db 401 KSLCNWMLT-----KKFY---TNDNSCNIGFLKLTQATINMEKK 438
 QY 1859 ELTSIHSQQLAFFALDFRAQHSEN-----DLEVGKTENCICLVLAMVUKSSEVFR 1913
 Db 439 QATTOATLFLMRWLISAFEFR-QYSEDNDKEDNNTHRLSSFHGCAIAFWMKNDKSFR 497
 QY 1914 PLFFKLFDWA-----KTEDAPKDRLLTFYNLADCIACBKLGIFTLEAGHLVVPFADT 1965
 Db 498 PLFANLVRWAVDGEATLKNEV-SRLLAFFFNKLQBLKSITSVFSYLLDPTSAL 555
 QY 1966 LXQVNISKTBAAFFESENDPEKCCCLLQFLNCNLKIFLDTOHRSKE-RAXAMMPJ 2024
 Db 556 L-----KRFSEGSLWATN-----LRRITLGLGSSFSKYDODDWSQCRFDSCPSL 603
 QY 2025 DOLENLRGSGEKFQFRVTKHILPCQAQFSVAMADSLWKLNQYI---LJKTRSSPKR 2081
 Db 604 SOLSN-----IEISIGKVLYKSVSTFVTDVSSBEYNETLVHLLIKYISNANENSAATK 656
 QY 2082 FAALITVLALAKLKENYVILPESIPIFLBLMEDCECEVHOCOK-TQOLETVLGEPL 2140
 Db 657 IWSITRKLTKFQKOMBQWLSQVLPYIABLEDDEVEVMEVERGLVRVENLGEPL 715
 QY 2141 QSY 2143
 Db 717 DRY 719

RESULT 2
 US-09-248-796A-15108
 Sequence 15108 Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15108 LENGTH: 2954

TYPE: PRT

ORGANISM: Xenopus sp.

FEATURE: OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E) OTHER INFORMATION: member of the kinesin superfamily of microtubule motor proteins

FEATURE: OTHER INFORMATION: motor proteins

NAME/KEY: DOMAIN

LOCATION: (1)..(472)

FEATURE: OTHER INFORMATION: kinesin like motor domain

NAME/KEY: DOMAIN

LOCATION: (473)..(2752)

FEATURE: OTHER INFORMATION: rod domain

FEATURE: NAME/KEY: DOMAIN

LOCATION: (2753)..(2954)

FEATURE: OTHER INFORMATION: tail domain

US-09-150-867-1

Query Match 2.5%; Score 272.5; DB 2; Length 2954; Best local Similarity 18.7%; Pred. No. 3.1e-12; Matches 415; Conservative 365; Mismatches 807; Indels 529; Gaps 96; Matches 415; Conservative 365; Mismatches 807; Indels 529; Gaps 96;

QY 1 MTSIQAQQLRQLAPQSDASLRL-----LMDNFNDNIL---ENETKREA-----DLERSLKENQ 744
 Db 702 MAEKONALBELA-----LMDNFNDNIL---ENETKREA-----DLERSLKENQ 744
 QY 61 SIEGFEARPLSOLAKTLERSVQKAVN-----KOLDENISLELHLSPYF-----LWPA 110
 Db 745 ETNEFEI-----LEKETOKHEAQHQLIETGSLKLVENAMMNQNSEDLETKTKLKEQ 799
 QY 111 QKCLEWL-----IHRFHHLYNQDSLACVLPVPHETRIFVURVQOLKINNSHRW 160
 Db 840 -----KOS-----LSDAEAVTRDQAKESFLRSSENLELKEKMDTSNWNOKEKAASLFEK 890
 QY 53 EBLQGIDPSPEOFEAPLFSOLAKTLERSVQKAVNQKDENSILFLHISLSPYFLKPAOK 112
 Db 60 EDLGELDSRENKFKNTLFSTSVNIDRNLQTKDVSQDGNIDAFLTUVPGYIGTSSK 119
 QY 113 CLEMNIHREHHLYNQDSLACVLPVPHETRIFVURVQOLKINNSHRWFLPVR-QSY 171
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172 PLAKGTLITHCYKUDGFMD 191

Db 180 PPASSIL-----KGMSAMNF 194

RESULT 3
 US-09-150-867-1
 Sequence 1, Application US/09150867
 Patent No. 6645748

GENERAL INFORMATION:

APPLICANT: Wood, Kenneth W.

APPLICANT: Sakowicz, Roman

APPLICANT: Goldstein, Lawrence S.B.

APPLICANT: Cleveland, Don W.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: End-Directed Microtubule Motor Required for File Reference: 18557C-000110S

CURRENT FILING NUMBER: US/09/150, 867

CURRENT FILING DATE: 1998-09-10

EARLIER APPLICATION NUMBER: US 60/058, 645

EARLIER FILING DATE: 1997-09-11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 2954

TYPE: PRT

ORGANISM: Xenopus sp.

FEATURE: OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E) OTHER INFORMATION: member of the kinesin superfamily of microtubule motor proteins

FEATURE: OTHER INFORMATION: motor proteins

NAME/KEY: DOMAIN

LOCATION: (1)..(472)

FEATURE: OTHER INFORMATION: kinesin like motor domain

NAME/KEY: DOMAIN

LOCATION: (473)..(2752)

FEATURE: OTHER INFORMATION: rod domain

FEATURE: NAME/KEY: DOMAIN

LOCATION: (2753)..(2954)

FEATURE: OTHER INFORMATION: tail domain

US-09-150-867-1

Query Match 2.5%; Score 272.5; DB 2; Length 2954; Best local Similarity 18.7%; Pred. No. 3.1e-12; Matches 415; Conservative 365; Mismatches 807; Indels 529; Gaps 96; Matches 415; Conservative 365; Mismatches 807; Indels 529; Gaps 96;

QY 1 MTSIQAQQLRQLAPQSDASLRL-----LMDNFNDNIL---ENETKREA-----DLERSLKENQ 744
 Db 702 MAEKONALBELA-----LMDNFNDNIL---ENETKREA-----DLERSLKENQ 744
 QY 61 SIEGFEARPLSOLAKTLERSVQKAVN-----KOLDENISLELHLSPYF-----LWPA 110
 Db 745 ETNEFEI-----LEKETOKHEAQHQLIETGSLKLVENAMMNQNSEDLETKTKLKEQ 799
 QY 111 QKCLEWL-----IHRFHHLYNQDSLACVLPVPHETRIFVURVQOLKINNSHRW 160
 Db 840 -----KOS-----LSDAEAVTRDQAKESFLRSSENLELKEKMDTSNWNOKEKAASLFEK 890
 QY 199 SVKV-FAEXPGSSAQLRVIL-AFYASTIVSVAEVDVSDNT---IAKLFPYIQLKL 251
 Db 891 OLETEKSNKKMADLQKELQSAFNEINYLNLQSLAGKVPDRDLISRVELEKKSPESKLE 950
 QY 252 SISDYPYATYMICOLSVKVMNTENFLSLSQIOIKLTKPSLKGSLCIVLQHQ 311
 Db 951 KALBEKNALENVTCLSVYKFLNE-VECLKNOQISKASEEMILKQIGEBSASII--S 1005

GenCore version 5.1.9
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Om protein - protein search, using sw model

Run on: June 29, 2006, 00:52:34 ; Search time 134.107 Seconds

(without alignments) 7405.549 Million cell updates/sec

Title: US-09-603-665-5

Perfect score: 10803

Sequence: 1 MTLAQLQLRQLALPOSDSL.....CQKTIQOLETVLGEPLQSYF 2144

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2037797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2037797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /EMC_Celerra_SIDS3ptodata/2/pubpbaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3ptodata/2/pubpbaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3ptodata/2/pubpbaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3ptodata/2/pubpbaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3ptodata/2/pubpbaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Length DB ID Description

Result No. Score Match Length DB ID Description

Sequence 215, App
Sequence 36864, A
Sequence 256711, App
Sequence 214, App
Sequence 1, Appli
Sequence 749, Appli
Sequence 9, Appli
Sequence 9003, App
Sequence 10683, App
Sequence 11, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 20, Appli
Sequence 1, Appli
Sequence 41, Appli
Sequence 2, Appli
Sequence 338, App

ALIGNMENTS

RESULT 1
US-10-745-237-230

; Sequence 230, Application US/10745237
; Publication No. US20050227301A1

; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited

; APPLICANT: Glover, David
; APPLICANT: Bell, Graham

; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol

; TITLE OF INVENTION: Cell-Cycle Progression Proteins

; FILE REFERENCE: P015819MO CYK

; CURRENT APPLICATION NUMBER: US/10/745, 237

; CURRENT FILING DATE: 2003-12-23

; PRIOR APPLICATION NUMBER: US 60/439, 123

; PRIOR FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: US 60/468, 492

; PRIOR FILING DATE: 2003-05-06

; NUMBER OF SEQ ID NOS: 600

; SEQ ID NO: 230
; LENGTH: 2144

; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE: OTHER INFORMATION: 09H583

US-10-745-237-230

Query Match 99.9% ; Score 10799 ; DB 5 ; Length 2144 ;

Best Local Similarity 99.8% ; Pred. No. 0 ; Mismatches 0 ; Indels 4 ; Gaps 0 ;

Matches 2140 ; Conservative 0 ;

Sequence 177, App

Sequence 3300, App

Sequence 729, App

Sequence 36, Appli

Sequence 25518, A

Sequence 158, App

Sequence 189782,

Sequence 8388, App

Sequence 3388, App

Sequence 7616, App

Sequence 248111, App

Sequence 2412, App

Sequence 295784, App

Sequence 44447, A

Sequence 37036, A

Sequence 2, Appli

Sequence 4, Appli

Sequence 6, Appli

Sequence 8, Appli

QY

1 MTLAQLQLRQLALPOSDSLRSDEVASLFPKEATIDRTAFAFGCTGIGELGIDP 60

1 MTLAQLQLRQLALPOSDSLRSDEVASLFPKEATIDRTAFAFGCTGIGELGIDP 60

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61 SREQFAPLFSQALKTERSVQTKAVKQDLENIFLHSPPYFLKPAQKLEWLR 120

121 FHILHNQDSLJACVLPYHETRIVFVQLIKINNSKRNHRWFLPPVQSGVPLAKPLIT 180

121 FHILHNQDSLJACVLPYHETRIVFVQLIKINNSKRNHRWFLPPVQSGVPLAKPLIT 180

121 FHILHNQDSLJACVLPYHETRIVFVQLIKINNSKRNHRWFLPPVQSGVPLAKPLIT 180

181 HCYKDQGFMDCISLUTSKVFAEPGSSQQLRVLIAFVASTIVSALVAEDVSDNIA 240

181 HCYKDQGFMDCISLUTSKVFAEPGSSQQLRVLIAFVASTIVSALVAEDVSDNIA 240

241 KLFPIYQGKISLPSLPPYRATMTCQISVKTMENTFVNLASQIKLTIKPSLKD 300

Db 241 KLFPPYIQQKLKSSLPDYRAATYMICQISVKVMENTFVNLSASQIKLTKPLSIKG 300 Qy 1381 SYFVDALPHVPHERRPLPILVOLVDTGAEKFWILLLFCYVTKVLAAYGEKDAIL 1440
 301 LSCLIVLULORQKESLGKPPFLCNVNDLITLHGJSETYDVSPLRQYMLFLVWVITH 360 Db 1381 SYFVDALPHVPHERRPLPILVOLVDTGAEKFWILLLFCYVTKVLAAYGEKDAIL 1440
 301 LSCLIVLULORQKESLGKPPFLCNVNDLITLHGJSETYDVSPLRQYMLFLVWVITH 360 Qy 1441 EADTEPWSVCBFSVQHQSILMNLQYLLKPEEKEETPKAVFNSKSEOBMLOVF 1 500
 361 HVTGEGETECDGQYKHLRALKISLKNLHLLASLFFEEYTSYSSQEMDSNKVL 420 Db 1441 EADTEPWSVCBFSVQHQSILMNLQYLLKPEEKEETPKAVFNSKSEOBMLOVF 1 500
 361 HVTGEGETECDGQYKHLRALKISLKNLHLLASLFFEEYTSYSSQEMDSNKVL 420 Qy 1501 NVEHTTKQLRQKPLSVFMSOLLSNNPLKUVESGGPPLKGEBERLLTUVGISA 1 560
 421 LNSOFLPLRULRLESKRYPTDVLVIREBHLKEDIADLKQELPHQFVSLSTSGGKQPLADSD 480 Db 1501 NVEHTTKQLRQKPLSVFMSOLLSNNPLKUVESGGPPLKGEBERLLTUVGISA 1 560
 421 LNSOFLPLRULRLESKRYPTDVLVIREBHLKEDIADLKQELPHQFVSLSTSGGKQPLADSD 480 Qy 1561 VAGSMERNAKDTKTVFWRALLSKAYDLDKVNALLPFTFIVTRGLVGNPLPSVRKAL 1620
 481 TSLMSLNHLPLAPTRILAMMHLKMKTSKEGVDFEKAVALRGDNDIVVLSA 540 Db 1561 VAGSMERNAKDTKTVFWRALLSKAYDLDKVNALLPFTFIVTRGLVGNPLPSVRKAL 1620
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 601 VCLJFVWVNNDDTSEAMKIAVYISKSGICSLHLLRGMEALENVIAKSTKPGKIGA 660 Db 1681 FGAENDPDPVPLVXTAVKLIAPERKEKEONVLSALCTAEVSTLEAIPOLPSLMSL 1740
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 661 NOKMELLAADNINGDPSMILKOMVDLISYGEEFNLKQVTFVILSVLSCSSLKE 720 Db 1741 LTMKNTSISLVSSEVYLISALALQVETPLPHRISPMLGJSQVHETKISEMGAS 1800
 661 NOKMELLAADNINGDPSMILKOMVDLISYGEEFNLKQVTFVILSVLSCSSLKE 720 Qy 1801 QANRILTSKLTATLARVLLPAIKTYKQIKRNWKHMMGPMSILOEHIGMKKEI 1860
 721 THPPAIRVFLVSLQKIKKLESVITAVEIPSEWHTFLMLORGIPVBLWAVIEENSTOR 780 Db 1801 QANRILTSKLTATLARVLLPAIKTYKQIKRNWKHMMGPMSILOEHIGMKKEI 1860
 721 THPPAIRVFLVSLQKIKKLESVITAVEIPSEWHTFLMLORGIPVBLWAVIEENSTOR 780 Qy 1861 TSHQQLTAFLAFLDPRACHSENDLEBEVGKTCIDCIVAMVTKLSFTFRFLPKLF 1920
 781 VAVEDSVFLVSLKKEIYALGAKPSPKGDJWNPOLKEDSRDYLILLGLEMMLNGA 840 Db 1861 TSHQQLTAFLAFLDPRACHSENDLEBEVGKTCIDCIVAMVTKLSFTFRFLPKLF 1920
 781 VAVEDSVFLVSLKKEIYALGAKPSPKGDJWNPOLKEDSRDYLILLGLEMMLNGA 840 Qy 1921 DWAKTEDAPKDLTFLPNLADCAEKLKGFLTFLAGHLYKPFADTLXQNSKTDFAFD 1980
 841 DAVHFRVLMKLFIKVHLEDVOLFKECSVLWVYSSISNPJCSVKVLTQALVYCAM 900 Db 1921 DWAKTEDAPKDLTFLPNLADCAEKLKGFLTFLAGHLYKPFADTLXQNSKTDFAFD 1980
 841 DAVHFRVLMKLFIKVHLEDVOLFKECSVLWVYSSISNPJCSVKVLTQALVYCAM 900 Qy 1981 SENDPEKCCLLQFLINCLYKIFLFTQHISKERAAXALMPLVQLENLIGGEEKFOER 2040
 901 LSSQKTOCKHOLASISSPVVTSLLINLGLSPVKEVRRAIQCLOALGSVASYPLFIDHLI 960 Db 1981 SENDPEKCCLLQFLINCLYKIFLFTQHISKERAAXALMPLVQLENLIGGEEKFOER 2040
 901 LSSQKTOCKHOLASISSPVVTSLLINLGLSPVKEVRRAIQCLOALGSVASYPLFIDHLI 960 Qy 2041 VTKHLPLCIAFSVANADDSWKPLNYQILKTRSSPKURFALITVLAEKUNYI 2100
 961 SKAEETSDAAVYQDIALTFLFELOREKKLKHQKUSSETKOLLSVCYSCYIADLMK 1020 Db 2041 VTKHLPLCIAFSVANADDSWKPLNYQILKTRSSPKURFALITVLAEKUNYI 2100
 961 SKAEETSDAAVYQDIALTFLFELOREKKLKHQKUSSETKOLLSVCYSCYIADLMK 1020 Qy 2101 VLPESITPLFLARLMEDECEEVHOCQTKIQOLETVLGEPLSYF 2144
 1021 VLGONGNEMVUSQOLPMAQLEKIQKEPTAVKUDEAMVHLUTLGKNEFSLNEDPK 1080 Db 2101 VLPESITPLFLARLMEDECEEVHOCQTKIQOLETVLGEPLSYF 2144
 1021 VLGONGNEMVUSQOLPMAQLEKIQKEPTAVKUDEAMVHLUTLGKNEFSLNEDPK 1080 Qy 2101 VLPESITPLFLARLMEDECEEVHOCQTKIQOLETVLGEPLSYF 2144
 Db RESULT 2
 US-11-124-368A-277
 ; Sequence 277, Application US/11124368A
 ; Publication No. US20050287559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: James J. Devlin
 ; APPLICANT: May Luke
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
 ; FILE REFERENCE: C101524
 ; CURRENT APPLICATION NUMBER: US/11/124,368A
 ; CURRENT FILING DATE: 2005-05-09
 ; CURRENT FILING NUMBER: US 60/568,845
 ; PRIORITY FILING DATE: 2004-05-07
 ; PRIORITY FILING NUMBER: US 60/625,936
 ; PRIORITY FILING DATE: 2004-11-09
 ; NUMBER OF SEQ ID NOS: 2112
 ; SOFTWARE: FastSEQ for Windows Version 4.0

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GenCore version 5.1.9

Om protein - protein search, using sw model

Run on: June 29, 2006, 00:53:49 ; Search time 11.932 Seconds

Perfect score: 10803 Sequence: 1 MTLAQQLQLRQLPQSDASL.....CQKTIQOLETVLGEPLQSYF 2144

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New: *
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description	ALIGMENTS
1	3694	34.2	734	US-11-293-697-3300	RESULT 1 US-11-293-697-3300 ; Sequence 3300, Application US/11293697 ; Publication No. US20060105376A1
2	235	2.2	3113	6 US-10-505-928-325	GENERAL INFORMATION: ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: Novel full length cDNA ; FILE REFERENCE: H1-A016 ; CURRENT APPLICATION NUMBER: US/11/293, 697 ; CURRENT FILING DATE: 2005-12-05 ; PRIORITY APPLICATION NUMBER: US/10/108, 260 ; PRIORITY FILING DATE: 2002-03-28 ; NUMBER OF SEQ ID NOS: 5458 ; SOFTWARE: PatentIn Ver. 2.1 ; SBQ ID NO: 3300 ; LENGTH: 734 ; TYPE: PRT ; ORGANISM: Homo sapiens
3	207.5	1.9	2209	7 US-11-301-1903	
4	205	1.9	93	6 US-10-449-902-34905	
5	188.5	1.7	1328	6 US-10-504-973-32	
6	184.5	1.7	9535	6 US-10-471-571A-4496	
7	179	1.7	1206	7 US-10-449-902-43305	
8	175	1.6	1205	7 US-11-293-697-2967	
9	175	1.6	1842	6 US-10-511-937-2929	
10	173.5	1.6	1176	6 US-10-449-902-46322	
11	171	1.6	1325	6 US-10-449-902-51794	
12	166	1.5	1346	6 US-10-449-902-55021	
13	163.5	1.5	281	6 US-10-505-928-100	
14	161	1.5	1281	6 US-11-449-902-51746	
15	159.5	1.5	2671	6 US-10-505-928-784	
16	158.5	1.5	1116	6 US-10-449-902-7106	
17	157.5	1.5	980	7 US-11-202-296	
18	155	1.4	764	6 US-10-449-902-45961	
19	155	1.4	1230	7 US-11-289-102-378	
20	152.5	1.4	748	6 US-11-449-902-53645	
21	152	1.4	2354	7 US-11-289-102-242	
22	152	1.4	1368	7 US-11-283-329-666	
23	151.5	1.4	1120	6 US-10-205-928-213	
24	150	1.4	1050	6 US-10-471-571A-4624	
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 Db 361 RYTGEEETGMDQOIKYRHEALITKISLKNNDLHLLASLUREEYSSYSSOREMDNKVL 420
 Qy 421 LNEQFLPLIRLIESKPYRTDVLLEBLKETADLKKOBLFQFVSLSTSGCKYQFLADSD 480
 Db 421 LNEQFLPLIRLIESKPYRTDVLLEBLKETADLKKOBLFQFVSLSTSGCKYQFLADSD 480
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 Db 601 VCLLPFWVNNDDTESAEMKAIYLSKSGICSLHPLRGWEBALENVIKSTPKGLIGVA 660
 Qy 661 NOKMIELADNINGDPSMLKRNVEDLISVGEBESENPLKQVTFHVLISVLSVSCSSLKE 720
 Db 661 NOKMIELADNINGDPSMLKRNVEDLISVGEBESENPLKQVTFHVLISVLSVSCSSLKE 720
 Qy 721 THFPAIRVFSLQ 734
 Db 721 THFPAIRVFSLQ 734

RESULT 2
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 ;Sequence 325, Application US/10505928
 ;Publication No. US20060088532A1
 ;GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505,928
 ; PRIOR FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/363, 019
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: Patentin 3.2
 ; SEQ ID NO: 325
 ; LENGTH: 3113
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-505-928-325
 ;Query Match 2.2%; Score 235; DB 6; Length 3113;
 ;Best Local Similarity 19.0%; Pred. No. 6e-05;
 ;Matches 427; Conservative 357; Mismatches 817; Indels 646; Gaps 101;

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 Qy 242 LPPYIQC-----GLKSSLPDYRATMICOISVKUTMENFVNLSLASQIKTL 290
 Db 786 ---FDDQPMAMHSFANTIGECDSPMSPERE---CRLEADQSPKNS----- 824
 Qy 291 TKIPSLTKDGSCLTIVLQROKP---ESLGKKPFPHCNVPDLITIUNGISE----- 339
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 Qy 340 -----TYDVSPLRITMLPHLVVSVIHHVTCERETGMDGOIKYRHEALITKISLKN 392
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 Qy 933 NHILDESLIKELOLISSETISL-EKEMESIISLANKREELT-QENTGILKEINASLQNEKMN 991

Qy 428 LIRLLESKYPRTDVLLEBLKETADLKKOBLFQFVSLSTSGCKYQFLA-----DSD 480
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 Qy 481 TSLMLSINHPLAPVRLAMNHKKIMKTSKEGVDESEFIKEAVLARLGGDDNDVVL 535
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 Qy 536 SAISAFEFKHFSEVETINSLNLFORALESKNGEVEVLIKAADILIKEELS-EN 592
 Db 1101 E---LETVOQALASEWTDN---QNNKSKSEAGG-----LKQEMITLKBEQ 1138
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 Db 1139 NKMKEV-----NDLQNEBOLMKVMKVKECONLE-----SEPIRNSKERE 1181
 Qy 653 PGKLIGVANQ-----KMFELLADNINGDPSMLKRNVEDLISVGEBESENPLKQVTFHVLISVLSVSCSSLKE 720
 Db 1182 SER-----NQCNFKPQMDLBVKRISDYNALQVOLEMAMRNKLKLOESEKEKECLOHE 1236
 Qy 687 LISV-GEESFFNLKOKVTFHVLISVLSVSCSSLKE-----PFAI-----RVSFLQK 735
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 Qy 796 PTIALK-----APKSFPKGDIWINNPEQLK-----EDSDYDYLHLLIGLFEMM 836
 Db 1341 LINNEVKILNDGSLGLHGLGELVEDIPGGEFGEQPNQEPVSLAPLDESNSYEHTLSDKEVQ 1400
 Qy 837 LINGADAVHFRVFLMFLKIFKHLDF-----OLFKFCSTLWITGSSL-----SNPIN 882
 Db 1401 M-----HEALQOKFLSLOSEHKTLDHOCQMSKMSBLQTYVDSLKAENLVLSTLN 1454
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 Qy 990 LKSHQKLSLETKLNLSCVYSCPSYIAKDEMVKLUGVNGR-----MVLSQLPMAEOLKE 1044
 Db 1565 LEEKMEQSGIMKIN-----KEIQLEOLISSERBQBLDCLRKQYLSENEQWOQK 1611
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 Qy 1251 TKQILSCLINICOKLSPROGKPKDILBEEKFNVELIVQCTIRSEMPOTHHLILGT 1310
 Db 1812 LOEVOLMKTIAECALEKIVGELKKNSDE-----KUBYFSCDHQELLQVET 1861
 Qy 1311 VAGJFPDKVHNINMSIFTPGANWRLLDTYSFQVINKVWVMPALQDSG---DSI 1366
 Db 1862 SEGJNSDLEMHADKSSREPDIGNTAVKUNDWKERFLDVENTE---SRIRSEKASTERHE 1918
 Qy 1367 FVSRNVEITV-----KLSVFDALPHVPERRLPILVQI-----VDTLGAEK 1410